

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
20 October 2005 (20.10.2005)

PCT

(10) International Publication Number
WO 2005/098047 A2

(51) International Patent Classification⁷: **C12Q 1/68**

92009 (US). LARSON, Brons, M. [US/US]; 10657 Birch Bluff Avenue, San Diego, CA 92131 (US). LEIGHTON, Terrance [US/US]; Suite F, 3589 Walnut Street, Lafayette, CA 94549 (US).

(21) International Application Number:
PCT/US2005/005356

(22) International Filing Date: 18 February 2005 (18.02.2005)

(74) Agent: LEGAARD, Paul, K.; Cozen O'Connor, 1900 Market Street, Philadelphia, PA 19103 (US).

(25) Filing Language: English

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(26) Publication Language: English

(30) Priority Data:
60/545,425 18 February 2004 (18.02.2004) US
60/559,754 5 April 2004 (05.04.2004) US
60/632,862 3 December 2004 (03.12.2004) US
60/639,068 22 December 2004 (22.12.2004) US
60/648,188 28 January 2005 (28.01.2005) US

(71) Applicants (for all designated States except US): ISIS PHARMACEUTICALS, INC. [US/US]; 1896 Rutherford Road, Carlsbad, CA 92008 (US). SCIENCE APPLICATIONS INTERNATIONAL CORPORATION [US/US]; 10260 Campus Point Drive, MSC4, San Diego, CA 92121 (US).

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (for US only): SAMPATH, Rangarajan [US/US]; 12223 Mannix Road, San Diego, CA 92129 (US). HALL, Thomas, A. [US/US]; 5239 Wohlford Street, Oceanside, CA 92056 (US). ECKER, David, J. [US/US]; 1041 Saxony Road, Encinitas, CA 92024 (US). ESCHOO, Mark, W. [US/US]; 615 Glenmont Drive, Solana Beach, CA 92075 (US). MASSIRE, Christian [US/US]; 7498 Altiva Place, Carlsbad, CA

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: COMPOSITIONS FOR USE IN IDENTIFICATION OF BACTERIA

(57) Abstract: The present invention provides oligonucleotide primers and compositions and kits containing the same for rapid identification of bacteria by amplification of a segment of bacterial nucleic acid followed by molecular mass analysis.

WO 2005/098047 A2

COMPOSITIONS FOR USE IN IDENTIFICATION OF BACTERIA

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims the benefit of priority to: U.S. Provisional Application Serial No. 60/545,425 filed February 18, 2004, U.S. Provisional Application Serial No. 60/559,754, filed April 5, 2004, U.S. Provisional Application Serial No. 60/632,862, filed December 3, 2004, U.S. Provisional Application Serial No. 60/639,068, filed December 22, 2004, and U.S. Provisional Application Serial No. 60/648,188, filed January 28, 2005, each of which is incorporated herein by reference in its entirety.

STATEMENT OF GOVERNMENT SUPPORT

[0002] This invention was made with United States Government support under DARPA/SPO contract BAA00-09. The United States Government may have certain rights in the invention.

FIELD OF THE INVENTION

[0003] The present invention relates generally to the field of genetic identification of bacteria and provides nucleic acid compositions and kits useful for this purpose when combined with molecular mass analysis.

BACKGROUND OF THE INVENTION

[0004] A problem in determining the cause of a natural infectious outbreak or a bioterrorist attack is the sheer variety of organisms that can cause human disease. There are over 1400 organisms infectious to humans; many of these have the potential to emerge suddenly in a natural epidemic or to be used in a malicious attack by bioterrorists (Taylor et al. Philos. Trans. R. Soc. London B. Biol. Sci., 2001, 356, 983-989). This number does not include numerous strain variants, bioengineered versions, or pathogens that infect plants or animals.

[0005] Much of the new technology being developed for detection of biological weapons incorporates a polymerase chain reaction (PCR) step based upon the use of highly specific primers and probes designed to selectively detect certain pathogenic organisms. Although this approach is appropriate for the most obvious bioterrorist organisms, like smallpox and anthrax, experience has shown that it is very difficult to predict which of hundreds of possible pathogenic organisms might be employed in a terrorist attack. Likewise, naturally emerging human disease that has caused devastating consequence in public health has come from unexpected families of

bacteria, viruses, fungi, or protozoa. Plants and animals also have their natural burden of infectious disease agents and there are equally important biosafety and security concerns for agriculture.

[0006] A major conundrum in public health protection, biodefense, and agricultural safety and security is that these disciplines need to be able to rapidly identify and characterize infectious agents, while there is no existing technology with the breadth of function to meet this need. Currently used methods for identification of bacteria rely upon culturing the bacterium to effect isolation from other organisms and to obtain sufficient quantities of nucleic acid followed by sequencing of the nucleic acid, both processes which are time and labor intensive.

[0007] Mass spectrometry provides detailed information about the molecules being analyzed, including high mass accuracy. It is also a process that can be easily automated. DNA chips with specific probes can only determine the presence or absence of specifically anticipated organisms. Because there are hundreds of thousands of species of benign bacteria, some very similar in sequence to threat organisms, even arrays with 10,000 probes lack the breadth needed to identify a particular organism.

[0008] There is a need for a method for identification of bioagents which is both specific and rapid, and in which no culture or nucleic acid sequencing is required. Disclosed in U.S. Patent Application Serial Nos: 09/798,007, 09/891,793, 10/405,756, 10/418,514, 10/660,997, 10/660,122, 10/660,996, 10/728,486, 10/754,415 and 10/829,826, each of which is commonly owned and incorporated herein by reference in its entirety, are methods for identification of bioagents (any organism, cell, or virus, living or dead, or a nucleic acid derived from such an organism, cell or virus) in an unbiased manner by molecular mass and base composition analysis of "bioagent identifying amplicons" which are obtained by amplification of segments of essential and conserved genes which are involved in, for example, translation, replication, recombination and repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, energy generation, uptake, secretion and the like. Examples of these proteins include, but are not limited to, ribosomal RNAs, ribosomal proteins, DNA and RNA polymerases, elongation factors, tRNA synthetases, protein chain initiation factors, heat shock protein groEL, phosphoglycerate kinase, NADH dehydrogenase, DNA ligases, DNA gyrases and DNA topoisomerases, metabolic enzymes, and the like.

[0009] To obtain bioagent identifying amplicons, primers are selected to hybridize to conserved sequence regions which bracket variable sequence regions to yield a segment of nucleic acid which can be amplified and which is amenable to methods of molecular mass analysis. The variable sequence regions provide the variability of molecular mass which is used for bioagent identification. Upon amplification by PCR or other amplification methods with the specifically chosen primers, an amplification product that represents a bioagent identifying amplicon is obtained. The molecular mass of the amplification product, obtained by mass spectrometry for example, provides the means to uniquely identify the bioagent without a requirement for prior knowledge of the possible identity of the bioagent. The molecular mass of the amplification product or the corresponding base composition (which can be calculated from the molecular mass of the amplification product) is compared with a database of molecular masses or base compositions and a match indicates the identity of the bioagent. Furthermore, the method can be applied to rapid parallel analyses (for example, in a multi-well plate format) the results of which can be employed in a triangulation identification strategy which is amenable to rapid throughput and does not require nucleic acid sequencing of the amplified target sequence for bioagent identification.

[0010] The result of determination of a previously unknown base composition of a previously unknown bioagent (for example, a newly evolved and heretofore unobserved bacterium or virus) has downstream utility by providing new bioagent indexing information with which to populate base composition databases. The process of subsequent bioagent identification analyses is thus greatly improved as more base composition data for bioagent identifying amplicons becomes available.

[0011] The present invention provides oligonucleotide primers and compositions and kits containing the oligonucleotide primers, which define bacterial bioagent identifying amplicons and, upon amplification, produce corresponding amplification products whose molecular masses provide the means to identify bacteria, for example, at and below the species taxonomic level.

SUMMARY OF THE INVENTION

[0012] The present invention provides primers and compositions comprising pairs of primers, and kits containing the same for use in identification of bacteria. The primers are designed to produce bacterial bioagent identifying amplicons of DNA encoding genes essential to life such as, for example, 16S and 23S rRNA, DNA-directed RNA polymerase subunits (rpoB and rpoC),

valyl-tRNA synthetase (valS), elongation factor EF-Tu (TufB), ribosomal protein L2 (rplB), protein chain initiation factor (infB), and spore protein (sspE). The invention further provides drill-down primers, compositions comprising pairs of primers and kits containing the same, which are designed to provide sub-species characterization of bacteria.

[0013] In particular, the present invention provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 80% to 100% sequence identity with SEQ ID NO: 26, or a composition comprising the same; an oligonucleotide primer 20 to 27 nucleobases in length comprising at least a 20 nucleobase portion of SEQ ID NO: 388, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 15 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 26, and a second oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 388.

[0014] The present invention also provides an oligonucleotide primer 22 to 35 nucleobases in length comprising SEQ ID NO: 29, or a composition comprising the same; an oligonucleotide primer 18 to 35 nucleobases in length comprising SEQ ID NO: 391, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 29, and a second oligonucleotide primer 13 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 391.

[0015] The present invention also provides an oligonucleotide primer 22 to 26 nucleobases in length comprising SEQ ID NO: 37, or a composition comprising the same; an oligonucleotide primer 20 to 30 nucleobases in length comprising SEQ ID NO: 362, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 37, and a second oligonucleotide primer 14 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 362.

[0016] The present invention also provides an oligonucleotide primer 13 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 48, or a composition comprising the same; an oligonucleotide primer 19 to 35 nucleobases in length comprising SEQ ID NO: 404, or a composition comprising the same; a composition comprising both primers; and

a composition comprising a first oligonucleotide primer 13 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 48, and a second oligonucleotide primer 14 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 404.

[0017] The present invention also provides an oligonucleotide primer 21 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 160, or a composition comprising the same; an oligonucleotide primer 21 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 515, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 21 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 160, and a second oligonucleotide primer 21 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 515.

[0018] The present invention also provides an oligonucleotide primer 17 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 261, or a composition comprising the same; an oligonucleotide primer 18 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 624, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 17 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 261, and a second oligonucleotide primer 18 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 624.

[0019] The present invention also provides an oligonucleotide primer 21 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 231, or a composition comprising the same; an oligonucleotide primer 17 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 591, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 21 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 231, and a second oligonucleotide primer 17 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 591.

[0020] The present invention also provides an oligonucleotide primer 14 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 349, or a composition

comprising the same; an oligonucleotide primer 17 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 711, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 14 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 349, and a second oligonucleotide primer 17 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 711.

[0021] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 240, or a composition comprising the same; an oligonucleotide primer 15 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 596, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 240, and a second oligonucleotide primer 15 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 596.

[0022] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 58, or a composition comprising the same; an oligonucleotide primer 21 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO:414, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 58, and a second oligonucleotide primer 15 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 414.

[0023] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 6, or a composition comprising the same; an oligonucleotide primer 16 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO:369, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 6, and a second oligonucleotide primer 15 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 369.

[0024] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 246, or a composition comprising the same; an oligonucleotide primer 19 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 602, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 246, and a second oligonucleotide primer 19 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 602.

[0025] The present invention also provides an oligonucleotide primer 21 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 256, or a composition comprising the same; an oligonucleotide primer 14 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 620, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 21 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 256, and a second oligonucleotide primer 14 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 620.

[0026] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 344, or a composition comprising the same; an oligonucleotide primer 18 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 700, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 344, and a second oligonucleotide primer 18 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 700.

[0027] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 235, or a composition comprising the same; an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 587, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of

SEQ ID NO: 235, and a second oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 587.

[0028] The present invention also provides an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 322, or a composition comprising the same; an oligonucleotide primer 19 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 686, or a composition comprising the same; a composition comprising both primers; and a composition comprising a first oligonucleotide primer 16 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 322, and a second oligonucleotide primer 19 to 35 nucleobases in length comprising between 70% to 100% sequence identity of SEQ ID NO: 686.

[0029] The present invention also provides compositions, such as those described herein, wherein either or both of the first and second oligonucleotide primers comprise at least one modified nucleobase, a non-templated T residue on the 5'-end, at least one non-template tag, or at least one molecular mass modifying tag, or any combination thereof.

[0030] The present invention also provides kits comprising any of the compositions described herein. The kits can comprise at least one calibration polynucleotide, or at least one ion exchange resin linked to magnetic beads, or both.

[0031] The present invention also provides methods for identification of an unknown bacterium. Nucleic acid from the bacterium is amplified using any of the compositions described herein to obtain an amplification product. The molecular mass of the amplification product is determined. Optionally, the base composition of the amplification product is determined from the molecular mass. The base composition or molecular mass is compared with a plurality of base compositions or molecular masses of known bacterial bioagent identifying amplicons, wherein a match between the base composition or molecular mass and a member of the plurality of base compositions or molecular masses identifies the unknown bacterium. The molecular mass can be measured by mass spectrometry. In addition, the presence or absence of a particular clade, genus, species, or sub-species of a bioagent can be determined by the methods described herein.

[0032] The present invention also provides methods for determination of the quantity of an unknown bacterium in a sample. The sample is contacted with any of the compositions described

herein and a known quantity of a calibration polynucleotide comprising a calibration sequence. Concurrently, nucleic acid from the bacterium in the sample is amplified with any of the compositions described herein and nucleic acid from the calibration polynucleotide in the sample is amplified with any of the compositions described herein to obtain a first amplification product comprising a bacterial bioagent identifying amplicon and a second amplification product comprising a calibration amplicon. The molecular mass and abundance for the bacterial bioagent identifying amplicon and the calibration amplicon is determined. The bacterial bioagent identifying amplicon is distinguished from the calibration amplicon based on molecular mass, wherein comparison of bacterial bioagent identifying amplicon abundance and calibration amplicon abundance indicates the quantity of bacterium in the sample. The method can also comprise determining the base composition of the bacterial bioagent identifying amplicon.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] Figure 1 is a representative pseudo-four dimensional plot of base compositions of bioagent identifying amplicons of enterobacteria obtained with a primer pair targeting the *rpoB* gene (primer pair no 14 (SEQ ID NOs: 37:362). The quantity each of the nucleobases A, G and C are represented on the three axes of the plot while the quantity of nucleobase T is represented by the diameter of the spheres. Base composition probability clouds surrounding the spheres are also shown.

[0034] Figure 2 is a representative diagram illustrating the primer selection process.

[0035] Figure 3 lists common pathogenic bacteria and primer pair coverage. The primer pair number in the upper right hand corner of each polygon indicates that the primer pair can produce a bioagent identifying amplicon for all species within that polygon.

[0036] Figure 4 is a representative 3D diagram of base composition (axes A, G and C) of bioagent identifying amplicons obtained with primer pair number 14 (a precursor of primer pair number 348 which targets 16S rRNA). The diagram indicates that the experimentally determined base compositions of the clinical samples (labeled NHRC samples) closely match the base compositions expected for *Streptococcus pyogenes* and are distinct from the expected base compositions of other organisms.

[0037] Figure 5 is a representative mass spectrum of amplification products representing bioagent identifying amplicons of *Streptococcus pyogenes*, *Neisseria meningitidis*, and *Haemophilus influenzae* obtained from amplification of nucleic acid from a clinical sample with primer pair number 349 which targets 23S rRNA. Experimentally determined molecular masses and base compositions for the sense strand of each amplification product are shown.

[0038] Figure 6 is a representative mass spectrum of amplification products representing a bioagent identifying amplicon of *Streptococcus pyogenes*, and a calibration amplicon obtained from amplification of nucleic acid from a clinical sample with primer pair number 356 which targets rplB. The experimentally determined molecular mass and base composition for the sense strand of the *Streptococcus pyogenes* amplification product is shown.

[0039] Figure 7 is a representative process diagram for identification and determination of the quantity of a bioagent in a sample.

[0040] Figure 8 is a representative mass spectrum of an amplified nucleic acid mixture which contained the Ames strain of *Bacillus anthracis*, a known quantity of combination calibration polynucleotide (SEQ ID NO: 741), and primer pair number 350 which targets the capC gene on the virulence plasmid pX02 of *Bacillus anthracis*. Calibration amplicons produced in the amplification reaction are visible in the mass spectrum as indicated and abundance data (peak height) are used to calculate the quantity of the Ames strain of *Bacillus anthracis*.

DESCRIPTION OF EMBODIMENTS

[0041] The present invention provides oligonucleotide primers which hybridize to conserved regions of nucleic acid of genes encoding, for example, proteins or RNAs necessary for life which include, but are not limited to: 16S and 23S rRNAs, RNA polymerase subunits, t-RNA synthetases, elongation factors, ribosomal proteins, protein chain initiation factors, cell division proteins, chaperonin groEL, chaperonin dnaK, phosphoglycerate kinase, NADH dehydrogenase, DNA ligases, metabolic enzymes and DNA topoisomerases. These primers provide the functionality of producing, for example, bacterial bioagent identifying amplicons for general identification of bacteria at the species level, for example, when contacted with bacterial nucleic acid under amplification conditions.

[0042] Referring to Figure 2, primers are designed as follows: for each group of organisms, candidate target sequences are identified (200) from which nucleotide alignments are created (210) and analyzed (220). Primers are designed by selecting appropriate priming regions (230) which allows the selection of candidate primer pairs (240). The primer pairs are subjected to *in silico* analysis by electronic PCR (ePCR) (300) wherein bioagent identifying amplicons are obtained from sequence databases such as, for example, GenBank or other sequence collections (310), and checked for specificity *in silico* (320). Bioagent identifying amplicons obtained from GenBank sequences (310) can also be analyzed by a probability model which predicts the capability of a particular amplicon to identify unknown bioagents such that the base compositions of amplicons with favorable probability scores are stored in a base composition database (325). Alternatively, base compositions of the bioagent identifying amplicons obtained from the primers and GenBank sequences can be directly entered into the base composition database (330). Candidate primer pairs (240) are validated by *in vitro* amplification by a method such as, for example, PCR analysis (400) of nucleic acid from a collection of organisms (410). Amplification products that are obtained are optionally analyzed to confirm the sensitivity, specificity and reproducibility of the primers used to obtain the amplification products (420).

[0043] Synthesis of primers is well known and routine in the art. The primers may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA). Any other means for such synthesis known in the art may additionally or alternatively be employed.

[0044] The primers can be employed as compositions for use in, for example, methods for identification of bacterial bioagents as follows. In some embodiments, a primer pair composition is contacted with nucleic acid of an unknown bacterial bioagent. The nucleic acid is amplified by a nucleic acid amplification technique, such as PCR for example, to obtain an amplification product that represents a bioagent identifying amplicon. The molecular mass of one strand or each strand of the double-stranded amplification product is determined by a molecular mass measurement technique such as, for example, mass spectrometry wherein the two strands of the double-stranded amplification product are separated during the ionization process. In some embodiments, the mass spectrometry is electrospray Fourier transform ion cyclotron resonance mass spectrometry (ESI-FTICR-MS) or electrospray time of flight mass spectrometry (ESI-TOF-MS). A list of possible base compositions can be generated for the molecular mass value

obtained for each strand and the choice of the correct base composition from the list is facilitated by matching the base composition of one strand with a complementary base composition of the other strand. The molecular mass or base composition thus determined is compared with a database of molecular masses or base compositions of analogous bioagent identifying amplicons for known bacterial bioagents. A match between the molecular mass or base composition of the amplification product from the unknown bacterial bioagent and the molecular mass or base composition of an analogous bioagent identifying amplicon for a known bacterial bioagent indicates the identity of the unknown bioagent.

[0045] In some embodiments, the primer pair used is one of the primer pairs of Table 1. In some embodiments, the method is repeated using a different primer pair to resolve possible ambiguities in the identification process or to improve the confidence level for the identification assignment.

[0046] In some embodiments, a bioagent identifying amplicon may be produced using only a single primer (either the forward or reverse primer of any given primer pair), provided an appropriate amplification method is chosen, such as, for example, low stringency single primer PCR (LSSP-PCR). Adaptation of this amplification method in order to produce bioagent identifying amplicons can be accomplished by one with ordinary skill in the art without undue experimentation.

[0047] In some embodiments, the oligonucleotide primers are "broad range survey primers" which hybridize to conserved regions of nucleic acid encoding RNA, such as ribosomal RNA (rRNA), of all, or at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% of known bacteria and produce bacterial bioagent identifying amplicons. As used herein, the term "broad range survey primers" refers to primers that bind to nucleic acid encoding rRNAs of all, or at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% known species of bacteria. In some embodiments, the rRNAs to which the primers hybridize are 16S and 23S rRNAs. In some embodiments, the broad range survey primer pairs comprise oligonucleotides ranging in length from 13 to 35 nucleobases, each of which have from 70% to 100% sequence identity with primer pair numbers 3, 10, 11, 14, 16, and 17 which consecutively correspond to SEQ ID NOs: 6:369, 26:388, 29:391, 37:362, 48:404, and 58:414.

[0048] In some cases, the molecular mass or base composition of a bacterial bioagent identifying amplicon defined by a broad range survey primer pair does not provide enough resolution to unambiguously identify a bacterial bioagent at the species level. These cases benefit from further analysis of one or more bacterial bioagent identifying amplicons generated from at least one additional broad range survey primer pair or from at least one additional "division-wide" primer pair (*vide infra*). The employment of more than one bioagent identifying amplicon for identification of a bioagent is herein referred to as "triangulation identification" (*vide infra*).

[0049] In other embodiments, the oligonucleotide primers are "division-wide" primers which hybridize to nucleic acid encoding genes of broad divisions of bacteria such as, for example, members of the *Bacillus/Clostridia* group or members of the α -, β -, γ -, and ϵ -proteobacteria. In some embodiments, a division of bacteria comprises any grouping of bacterial genera with more than one genus represented. For example, the β -proteobacteria group comprises members of the following genera: *Eikenella*, *Neisseria*, *Achromobacter*, *Bordetella*, *Burkholderia*, and *Ralstonia*. Species members of these genera can be identified using bacterial bioagent identifying amplicons generated with primer pair 293 (SEQ ID NOs: 344:700) which produces a bacterial bioagent identifying amplicon from the *tufB* gene of β -proteobacteria. Examples of genes to which division-wide primers may hybridize to include, but are not limited to: RNA polymerase subunits such as *rpoB* and *rpoC*, tRNA synthetases such as valyl-tRNA synthetase (*valS*) and aspartyl-tRNA synthetase (*aspS*), elongation factors such as elongation factor EF-Tu (*tufB*), ribosomal proteins such as ribosomal protein L2 (*rplB*), protein chain initiation factors such as protein chain initiation factor *infB*, chaperonins such as *groL* and *dnaK*, and cell division proteins such as peptidase *ftsH* (*hflB*). In some embodiments, the division-wide primer pairs comprise oligonucleotides ranging in length from 13 to 35 nucleobases, each of which have from 70% to 100% sequence identity with primer pair numbers 34, 52, 66, 67, 71, 72, 289, 290 and 293 which consecutively correspond to SEQ ID NOs: 160:515, 261:624, 231:591, 235:587, 349:711, 240:596, 246:602, 256:620, 344:700.

[0050] In other embodiments, the oligonucleotide primers are designed to enable the identification of bacteria at the clade group level, which is a monophyletic taxon referring to a group of organisms which includes the most recent common ancestor of all of its members and all of the descendants of that most recent common ancestor. The *Bacillus cereus* clade is an example of a bacterial clade group. In some embodiments, the clade group primer pairs comprise oligonucleotides ranging in length from 13 to 35 nucleobases, each of which have from 70% to

100% sequence identity with primer pair number 58 which corresponds to SEQ ID NOs: 322:686.

[0051] In other embodiments, the oligonucleotide primers are “drill-down” primers which enable the identification of species or “sub-species characteristics.” Sub-species characteristics are herein defined as genetic characteristics that provide the means to distinguish two members of the same bacterial species. For example, *Escherichia coli* O157:H7 and *Escherichia coli* K12 are two well known members of the species *Escherichia coli*. *Escherichia coli* O157:H7, however, is highly toxic due to its Shiga toxin gene which is an example of a sub-species characteristic. Examples of sub-species characteristics may also include, but are not limited to: variations in genes such as single nucleotide polymorphisms (SNPs), variable number tandem repeats (VNTRs). Examples of genes indicating sub-species characteristics include, but are not limited to, housekeeping genes, toxin genes, pathogenicity markers, antibiotic resistance genes and virulence factors. Drill-down primers provide the functionality of producing bacterial bioagent identifying amplicons for drill-down analyses such as strain typing when contacted with bacterial nucleic acid under amplification conditions. Identification of such sub-species characteristics is often critical for determining proper clinical treatment of bacterial infections. Examples of pairs of drill-down primers include, but are not limited to, a trio of primer pairs for identification of strains of *Bacillus anthracis*. Primer pair 24 (SEQ ID NOs: 97:451) targets the capC gene of virulence plasmid pX02, primer pair 30 (SEQ ID NOs: 127:482) targets the cyA gene of virulence plasmid pX02, and primer pair 37 (SEQ ID NOs: 174:530) targets the lef gene of virulence plasmid pX02. Additional examples of drill-down primers include, but are not limited to, six primer pairs that are used for determining the strain type of group A *Streptococcus*. Primer pair 80 (SEQ ID NOs: 310:668) targets the gki gene, primer pair 81 (SEQ ID NOs: 313:670) targets the gtr gene, primer pair 86 (SEQ ID NOs: 227:632) targets the murI gene, primer pair 90 (SEQ ID NOs: 285:640) targets the mutS gene, primer pair 96 (SEQ ID NOs: 301:656) targets the xpt gene, and primer pair 98 (SEQ ID NOs: 308:663) targets the yqiL gene.

[0052] In some embodiments, the primers used for amplification hybridize to and amplify genomic DNA, DNA of bacterial plasmids, or DNA of DNA viruses.

[0053] In some embodiments, the primers used for amplification hybridize directly to ribosomal RNA or messenger RNA (mRNA) and act as reverse transcription primers for obtaining DNA from direct amplification of bacterial RNA or rRNA. Methods of amplifying RNA using reverse

transcriptase are well known to those with ordinary skill in the art and can be routinely established without undue experimentation.

[0054] One with ordinary skill in the art of design of amplification primers will recognize that a given primer need not hybridize with 100% complementarity in order to effectively prime the synthesis of a complementary nucleic acid strand in an amplification reaction. Moreover, a primer may hybridize over one or more segments such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure or a hairpin structure). The primers of the present invention may comprise at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 99% sequence identity with any of the primers listed in Table 1. Thus, in some embodiments of the present invention, an extent of variation of 70% to 100%, or any range therebetween, of the sequence identity is possible relative to the specific primer sequences disclosed herein. Determination of sequence identity is described in the following example: a primer 20 nucleobases in length which is otherwise identical to another 20 nucleobase primer but having two non-identical residues has 18 of 20 identical residues ($18/20 = 0.9$ or 90% sequence identity). In another example, a primer 15 nucleobases in length having all residues identical to a 15 nucleobase segment of primer 20 nucleobases in length would have $15/20 = 0.75$ or 75% sequence identity with the 20 nucleobase primer.

[0055] Percent homology, sequence identity or complementarity, can be determined by, for example, the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison WI), using default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2, 482-489). In some embodiments, homology, sequence identity, or complementarity of primers with respect to the conserved priming regions of bacterial nucleic acid, is at least 70%, at least 80%, at least 90%, at least 92%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or is 100%.

[0056] In some embodiments, the primers described herein comprise at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 92%, at least 94%, at least 95%, at least 96%, at least 98%, or at least 99%, or 100% (or any range therebetween) sequence identity with the primer sequences specifically disclosed herein. Thus, for example, a primer may have between 70% and 100%, between 75% and 100%, between 80% and 100%, and between 95% and 100% sequence identity with SEQ ID NO: 26. Likewise, a primer may have similar sequence identity with any other primer whose nucleotide sequence is disclosed herein.

[0057] One with ordinary skill is able to calculate percent sequence identity or percent sequence homology and able to determine, without undue experimentation, the effects of variation of primer sequence identity on the function of the primer in its role in priming synthesis of a complementary strand of nucleic acid for production of an amplification product of a corresponding bioagent identifying amplicon.

[0058] In some embodiments of the present invention, the oligonucleotide primers are between 13 and 35 nucleobases in length (13 to 35 linked nucleotide residues). These embodiments comprise oligonucleotide primers 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 or 35 nucleobases in length, or any range therewithin.

[0059] In some embodiments, any given primer comprises a modification comprising the addition of a non-templated T residue to the 5' end of the primer (i.e., the added T residue does not necessarily hybridize to the nucleic acid being amplified). The addition of a non-templated T residue has an effect of minimizing the addition of non-templated A residues as a result of the non-specific enzyme activity of *Taq* polymerase (Magnuson et al. *Biotechniques*, 1996, 21, 700-709), an occurrence which may lead to ambiguous results arising from molecular mass analysis.

[0060] In some embodiments of the present invention, primers may contain one or more universal bases. Because any variation (due to codon wobble in the 3rd position) in the conserved regions among species is likely to occur in the third position of a DNA triplet, oligonucleotide primers can be designed such that the nucleotide corresponding to this position is a base which can bind to more than one nucleotide, referred to herein as a "universal nucleobase." For example, under this "wobble" pairing, inosine (I) binds to U, C or A; guanine (G) binds to U or C, and uridine (U) binds to U or C. Other examples of universal nucleobases include nitroindoles such as 5-nitroindole or 3-nitropyrrole (Loakes et al., *Nucleosides and Nucleotides*, 1995, 14, 1001-1003), the degenerate nucleotides dP or dK (Hill et al.), an acyclic nucleoside analog containing 5-nitroindazole (Van Aerschot et al., *Nucleosides and Nucleotides*, 1995, 14, 1053-1056) or the purine analog 1-(2-deoxy-β-D-ribofuranosyl)-imidazole-4-carboxamide (Sala et al., *Nucl. Acids Res.*, 1996, 24, 3302-3306).

[0061] In some embodiments, to compensate for the somewhat weaker binding by the "wobble" base, the oligonucleotide primers are designed such that the first and second positions of each triplet are occupied by nucleotide analogs which bind with greater affinity than the unmodified

nucleotide. Examples of these analogs include, but are not limited to, 2,6-diaminopurine which binds to thymine, 5-propynyluracil which binds to adenine and 5-propynylcytosine and phenoxazines, including G-clamp, which binds to G. Propynylated pyrimidines are described in U.S. Patent Nos. 5,645,985, 5,830,653 and 5,484,908, each of which is commonly owned and incorporated herein by reference in its entirety. Propynylated primers are described in U.S. Serial No. 10/294,203 which is also commonly owned and incorporated herein by reference in entirety. Phenoxazines are described in U.S. Patent Nos. 5,502,177, 5,763,588, and 6,005,096, each of which is incorporated herein by reference in its entirety. G-clamps are described in U.S. Patent Nos. 6,007,992 and 6,028,183, each of which is incorporated herein by reference in its entirety.

[0062] In some embodiments, non-template primer tags are used to increase the melting temperature (T_m) of a primer-template duplex in order to improve amplification efficiency. A non-template tag is at least three consecutive A or T nucleotide residues on a primer which are not complementary to the template. In any given non-template tag, A can be replaced by C or G and T can also be replaced by C or G. Although Watson-Crick hybridization is not expected to occur for a non-template tag relative to the template, the extra hydrogen bond in a G-C pair relative to a A-T pair confers increased stability of the primer-template duplex and improves amplification efficiency for subsequent cycles of amplification when the primers hybridize to strands synthesized in previous cycles.

[0063] In other embodiments, propynylated tags may be used in a manner similar to that of the non-template tag, wherein two or more 5-propynylcytidine or 5-propynyluridine residues replace template matching residues on a primer. In other embodiments, a primer contains a modified internucleoside linkage such as a phosphorothioate linkage, for example.

[0064] In some embodiments, the primers contain mass-modifying tags. Reducing the total number of possible base compositions of a nucleic acid of specific molecular weight provides a means of avoiding a persistent source of ambiguity in determination of base composition of amplification products. Addition of mass-modifying tags to certain nucleobases of a given primer will result in simplification of *de novo* determination of base composition of a given bioagent identifying amplicon (*vide infra*) from its molecular mass.

[0065] In some embodiments of the present invention, the mass modified nucleobase comprises one or more of the following: for example, 7-deaza-2'-deoxyadenosine-5-triphosphate, 5-iodo-2'-

deoxyuridine-5'-triphosphate, 5-bromo-2'-deoxyuridine-5'-triphosphate, 5-bromo-2'-deoxycytidine-5'-triphosphate, 5-iodo-2'-deoxycytidine-5'-triphosphate, 5-hydroxy-2'-deoxyuridine-5'-triphosphate, 4-thiothymidine-5'-triphosphate, 5-aza-2'-deoxyuridine-5'-triphosphate, 5-fluoro-2'-deoxyuridine-5'-triphosphate, O6-methyl-2'-deoxyguanosine-5'-triphosphate, N2-methyl-2'-deoxyguanosine-5'-triphosphate, 8-oxo-2'-deoxyguanosine-5'-triphosphate or thiothymidine-5'-triphosphate. In some embodiments, the mass-modified nucleobase comprises ^{15}N or ^{13}C or both ^{15}N and ^{13}C .

[0066] In some embodiments of the present invention, at least one bacterial nucleic acid segment is amplified in the process of identifying the bioagent. Thus, the nucleic acid segments that can be amplified by the primers disclosed herein and that provide enough variability to distinguish each individual bioagent and whose molecular masses are amenable to molecular mass determination are herein described as "bioagent identifying amplicons." The term "amplicon" as used herein, refers to a segment of a polynucleotide which is amplified in an amplification reaction. In some embodiments of the present invention, bioagent identifying amplicons comprise from about 45 to about 200 nucleobases (i.e. from about 45 to about 200 linked nucleosides), from about 60 to about 150 nucleobases, from about 75 to about 125 nucleobases. One of ordinary skill in the art will appreciate that the invention embodies compounds of 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, and 200 nucleobases in length, or any range therewithin. It is the combination of the portions of the bioagent nucleic acid segment to which the primers hybridize (hybridization sites) and the variable region between the primer hybridization sites that comprises the bioagent identifying amplicon. Since genetic data provide the underlying basis for identification of bioagents by the methods of the present invention, it is prudent to select segments of nucleic acids which ideally provide enough variability to distinguish each individual bioagent and whose molecular mass is amenable to molecular mass determination.

[0067] In some embodiments, bioagent identifying amplicons amenable to molecular mass determination which are produced by the primers described herein are either of a length, size or mass compatible with the particular mode of molecular mass determination or compatible with a means of providing a predictable fragmentation pattern in order to obtain predictable fragments of a length compatible with the particular mode of molecular mass determination. Such means of providing a predictable fragmentation pattern of an amplification product include, but are not limited to, cleavage with restriction enzymes or cleavage primers, for example. Methods of using restriction enzymes and cleavage primers are well known to those with ordinary skill in the art.

[0068] In some embodiments, amplification products corresponding to bacterial bioagent identifying amplicons are obtained using the polymerase chain reaction (PCR) which is a routine method to those with ordinary skill in the molecular biology arts. Other amplification methods may be used such as ligase chain reaction (LCR), low-stringency single primer PCR, and multiple strand displacement amplification (MDA) which are also well known to those with ordinary skill.

[0069] In the context of this invention, a “bioagent” is any organism, cell, or virus, living or dead, or a nucleic acid derived from such an organism, cell or virus. Examples of bioagents include, but are not limited to, cells, (including but not limited to human clinical samples, bacterial cells and other pathogens), viruses, fungi, protists, parasites, and pathogenicity markers (including but not limited to: pathogenicity islands, antibiotic resistance genes, virulence factors, toxin genes and other bioregulating compounds). Samples may be alive or dead or in a vegetative state (for example, vegetative bacteria or spores) and may be encapsulated or bioengineered. In the context of this invention, a “pathogen” is a bioagent which causes a disease or disorder.

[0070] In the context of this invention, the term “unknown bioagent” may mean either: (i) a bioagent whose existence is known (such as the well known bacterial species *Staphylococcus aureus* for example) but which is not known to be in a sample to be analyzed, or (ii) a bioagent whose existence is not known (for example, the SARS coronavirus was unknown prior to April 2003). For example, if the method for identification of coronaviruses disclosed in commonly owned U.S. Patent Serial No. 10/829,826 (incorporated herein by reference in its entirety) was to be employed prior to April 2003 to identify the SARS coronavirus in a clinical sample, both meanings of “unknown” bioagent are applicable since the SARS coronavirus was unknown to

science prior to April, 2003 and since it was not known what bioagent (in this case a coronavirus) was present in the sample. On the other hand, if the method of U.S. Patent Serial No. 10/829,826 was to be employed subsequent to April 2003 to identify the SARS coronavirus in a clinical sample, only the first meaning (i) of "unknown" bioagent would apply since the SARS coronavirus became known to science subsequent to April 2003 and since it was not known what bioagent was present in the sample.

[0071] The employment of more than one bioagent identifying amplicon for identification of a bioagent is herein referred to as "triangulation identification." Triangulation identification is pursued by analyzing a plurality of bioagent identifying amplicons selected within multiple core genes. This process is used to reduce false negative and false positive signals, and enable reconstruction of the origin of hybrid or otherwise engineered bioagents. For example, identification of the three part toxin genes typical of *B. anthracis* (Bowen et al., J. Appl. Microbiol., 1999, 87, 270-278) in the absence of the expected signatures from the *B. anthracis* genome would suggest a genetic engineering event.

[0072] In some embodiments, the triangulation identification process can be pursued by characterization of bioagent identifying amplicons in a massively parallel fashion using the polymerase chain reaction (PCR), such as multiplex PCR where multiple primers are employed in the same amplification reaction mixture, or PCR in multi-well plate format wherein a different and unique pair of primers is used in multiple wells containing otherwise identical reaction mixtures. Such multiplex and multi-well PCR methods are well known to those with ordinary skill in the arts of rapid throughput amplification of nucleic acids.

[0073] In some embodiments, the molecular mass of a particular bioagent identifying amplicon is determined by mass spectrometry. Mass spectrometry has several advantages, not the least of which is high bandwidth characterized by the ability to separate (and isolate) many molecular peaks across a broad range of mass to charge ratio (m/z). Thus, mass spectrometry is intrinsically a parallel detection scheme without the need for radioactive or fluorescent labels, since every amplification product is identified by its molecular mass. The current state of the art in mass spectrometry is such that less than femtomole quantities of material can be readily analyzed to afford information about the molecular contents of the sample. An accurate assessment of the molecular mass of the material can be quickly obtained, irrespective of whether the molecular

weight of the sample is several hundred, or in excess of one hundred thousand atomic mass units (amu) or Daltons.

[0074] In some embodiments, intact molecular ions are generated from amplification products using one of a variety of ionization techniques to convert the sample to gas phase. These ionization methods include, but are not limited to, electrospray ionization (ESI), matrix-assisted laser desorption ionization (MALDI) and fast atom bombardment (FAB). Upon ionization, several peaks are observed from one sample due to the formation of ions with different charges. Averaging the multiple readings of molecular mass obtained from a single mass spectrum affords an estimate of molecular mass of the bioagent identifying amplicon. Electrospray ionization mass spectrometry (ESI-MS) is particularly useful for very high molecular weight polymers such as proteins and nucleic acids having molecular weights greater than 10 kDa, since it yields a distribution of multiply-charged molecules of the sample without causing a significant amount of fragmentation.

[0075] The mass detectors used in the methods of the present invention include, but are not limited to, Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR-MS), time of flight (TOF), ion trap, quadrupole, magnetic sector, Q-TOF, and triple quadrupole.

[0076] In some embodiments, conversion of molecular mass data to a base composition is useful for certain analyses. As used herein, a "base composition" is the exact number of each nucleobase (A, T, C and G). For example, amplification of nucleic acid of *Neisseria meningitidis* with a primer pair that produces an amplification product from nucleic acid of 23S rRNA that has a molecular mass (sense strand) of 28480.75124, from which a base composition of A25 G27 C22 T18 is assigned from a list of possible base compositions calculated from the molecular mass using standard known molecular masses of each of the four nucleobases.

[0077] In some embodiments, assignment of base compositions to experimentally determined molecular masses is accomplished using "base composition probability clouds." Base compositions, like sequences, vary slightly from isolate to isolate within species. It is possible to manage this diversity by building "base composition probability clouds" around the composition constraints for each species. This permits identification of organisms in a fashion similar to sequence analysis. A "pseudo four-dimensional plot" (Figure 1) can be used to visualize the concept of base composition probability clouds. Optimal primer design requires optimal choice

of bioagent identifying amplicons and maximizes the separation between the base composition signatures of individual bioagents. Areas where clouds overlap indicate regions that may result in a misclassification, a problem which is overcome by a triangulation identification process using bioagent identifying amplicons not affected by overlap of base composition probability clouds.

[0078] In some embodiments, base composition probability clouds provide the means for screening potential primer pairs in order to avoid potential misclassifications of base compositions. In other embodiments, base composition probability clouds provide the means for predicting the identity of a bioagent whose assigned base composition was not previously observed and/or indexed in a bioagent identifying amplicon base composition database due to evolutionary transitions in its nucleic acid sequence. Thus, in contrast to probe-based techniques, mass spectrometry determination of base composition does not require prior knowledge of the composition or sequence in order to make the measurement.

[0079] The present invention provides bioagent classifying information similar to DNA sequencing and phylogenetic analysis at a level sufficient to identify a given bioagent. Furthermore, the process of determination of a previously unknown base composition for a given bioagent (for example, in a case where sequence information is unavailable) has downstream utility by providing additional bioagent indexing information with which to populate base composition databases. The process of future bioagent identification is thus greatly improved as more BCS indexes become available in base composition databases.

[0080] In one embodiment, a sample comprising an unknown bioagent is contacted with a pair of primers which provide the means for amplification of nucleic acid from the bioagent, and a known quantity of a polynucleotide that comprises a calibration sequence. The nucleic acids of the bioagent and of the calibration sequence are amplified and the rate of amplification is reasonably assumed to be similar for the nucleic acid of the bioagent and of the calibration sequence. The amplification reaction then produces two amplification products: a bioagent identifying amplicon and a calibration amplicon. The bioagent identifying amplicon and the calibration amplicon should be distinguishable by molecular mass while being amplified at essentially the same rate. Effecting differential molecular masses can be accomplished by choosing as a calibration sequence, a representative bioagent identifying amplicon (from a specific species of bioagent) and performing, for example, a 2 to 8 nucleobase deletion or

insertion within the variable region between the two priming sites. The amplified sample containing the bioagent identifying amplicon and the calibration amplicon is then subjected to molecular mass analysis by mass spectrometry, for example. The resulting molecular mass analysis of the nucleic acid of the bioagent and of the calibration sequence provides molecular mass data and abundance data for the nucleic acid of the bioagent and of the calibration sequence. The molecular mass data obtained for the nucleic acid of the bioagent enables identification of the unknown bioagent and the abundance data enables calculation of the quantity of the bioagent, based on the knowledge of the quantity of calibration polynucleotide contacted with the sample.

[0081] In some embodiments, the identity and quantity of a particular bioagent is determined using the process illustrated in Figure 7. For instance, to a sample containing nucleic acid of an unknown bioagent are added primers (500) and a known quantity of a calibration polynucleotide (505). The total nucleic acid in the sample is subjected to an amplification reaction (510) to obtain amplification products. The molecular masses of amplification products are determined (515) from which are obtained molecular mass and abundance data. The molecular mass of the bioagent identifying amplicon (520) provides the means for its identification (525) and the molecular mass of the calibration amplicon obtained from the calibration polynucleotide (530) provides the means for its identification (535). The abundance data of the bioagent identifying amplicon is recorded (540) and the abundance data for the calibration data is recorded (545), both of which are used in a calculation (550) which determines the quantity of unknown bioagent in the sample.

[0082] In some embodiments, construction of a standard curve where the amount of calibration polynucleotide spiked into the sample is varied, provides additional resolution and improved confidence for the determination of the quantity of bioagent in the sample. The use of standard curves for analytical determination of molecular quantities is well known to one with ordinary skill and can be performed without undue experimentation.

[0083] In some embodiments, multiplex amplification is performed where multiple bioagent identifying amplicons are amplified with multiple primer pairs which also amplify the corresponding standard calibration sequences. In this or other embodiments, the standard calibration sequences are optionally included within a single vector which functions as the

calibration polynucleotide. Multiplex amplification methods are well known to those with ordinary skill and can be performed without undue experimentation.

[0084] In some embodiments, the calibrant polynucleotide is used as an internal positive control to confirm that amplification conditions and subsequent analysis steps are successful in producing a measurable amplicon. Even in the absence of copies of the genome of a bioagent, the calibration polynucleotide should give rise to a calibration amplicon. Failure to produce a measurable calibration amplicon indicates a failure of amplification or subsequent analysis step such as amplicon purification or molecular mass determination. Reaching a conclusion that such failures have occurred is in itself, a useful event.

[0085] In some embodiments, the calibration sequence is inserted into a vector which then itself functions as the calibration polynucleotide. In some embodiments, more than one calibration sequence is inserted into the vector that functions as the calibration polynucleotide. Such a calibration polynucleotide is herein termed a "combination calibration polynucleotide." The process of inserting polynucleotides into vectors is routine to those skilled in the art and can be accomplished without undue experimentation. Thus, it should be recognized that the calibration method should not be limited to the embodiments described herein. The calibration method can be applied for determination of the quantity of any bioagent identifying amplicon when an appropriate standard calibrant polynucleotide sequence is designed and used. The process of choosing an appropriate vector for insertion of a calibrant is also a routine operation that can be accomplished by one with ordinary skill without undue experimentation.

[0086] The present invention also provides kits for carrying out, for example, the methods described herein. In some embodiments, the kit may comprise a sufficient quantity of one or more primer pairs to perform an amplification reaction on a target polynucleotide from a bioagent to form a bioagent identifying amplicon. In some embodiments, the kit may comprise from one to fifty primer pairs, from one to twenty primer pairs, from one to ten primer pairs, or from two to five primer pairs. In some embodiments, the kit may comprise one or more primer pairs recited in Table 1.

[0087] In some embodiments, the kit may comprise one or more broad range survey primer(s), division wide primer(s), clade group primer(s) or drill-down primer(s), or any combination thereof. A kit may be designed so as to comprise particular primer pairs for identification of a

particular bioagent. For example, a broad range survey primer kit may be used initially to identify an unknown bioagent as a member of the *Bacillus/Clostridia* group. Another example of a division-wide kit may be used to distinguish *Bacillus anthracis*, *Bacillus cereus* and *Bacillus thuringiensis* from each other. A clade group primer kit may be used, for example, to identify an unknown bacterium as a member of the *Bacillus cereus* clade group. A drill-down kit may be used, for example, to identify genetically engineered *Bacillus anthracis*. In some embodiments, any of these kits may be combined to comprise a combination of broad range survey primers and division-wide primers, clade group primers or drill-down primers, or any combination thereof, for identification of an unknown bacterial bioagent.

[0088] In some embodiments, the kit may contain standardized calibration polynucleotides for use as internal amplification calibrants. Internal calibrants are described in commonly owned U.S. Patent Application Serial No: 60/545,425 which is incorporated herein by reference in its entirety.

[0089] In some embodiments, the kit may also comprise a sufficient quantity of reverse transcriptase (if an RNA virus is to be identified for example), a DNA polymerase, suitable nucleoside triphosphates (including any of those described above), a DNA ligase, and/or reaction buffer, or any combination thereof, for the amplification processes described above. A kit may further include instructions pertinent for the particular embodiment of the kit, such instructions describing the primer pairs and amplification conditions for operation of the method. A kit may also comprise amplification reaction containers such as microcentrifuge tubes and the like. A kit may also comprise reagents or other materials for isolating bioagent nucleic acid or bioagent identifying amplicons from amplification, including, for example, detergents, solvents, or ion exchange resins which may be linked to magnetic beads. A kit may also comprise a table of measured or calculated molecular masses and/or base compositions of bioagents using the primer pairs of the kit.

[0090] In order that the invention disclosed herein may be more efficiently understood, examples are provided below. It should be understood that these examples are for illustrative purposes only and are not to be construed as limiting the invention in any manner. Throughout these examples, molecular cloning reactions, and other standard recombinant DNA techniques, were carried out according to methods described in Maniatis et al., Molecular Cloning - A Laboratory Manual,

2nd ed., Cold Spring Harbor Press (1989), using commercially available reagents, except where otherwise noted.

EXAMPLES

[0091] Example 1: Selection of Primers That Define Bioagent Identifying Amplicons

[0092] For design of primers that define bacterial bioagent identifying amplicons, relevant sequences from, for example, GenBank are obtained, aligned and scanned for regions where pairs of PCR primers would amplify products of about 45 to about 200 nucleotides in length and distinguish species from each other by their molecular masses or base compositions. A typical process shown in Figure 2 is employed.

[0093] A database of expected base compositions for each primer region is generated using an *in silico* PCR search algorithm, such as (ePCR). An existing RNA structure search algorithm (Macke et al., Nuc. Acids Res., 2001, 29, 4724-4735, which is incorporated herein by reference in its entirety) has been modified to include PCR parameters such as hybridization conditions, mismatches, and thermodynamic calculations (SantaLucia, Proc. Natl. Acad. Sci. U.S.A., 1998, 95, 1460-1465, which is incorporated herein by reference in its entirety). This also provides information on primer specificity of the selected primer pairs.

[0094] Table 1 represents a collection of primers (sorted by forward primer name) designed to identify bacteria using the methods herein described. The forward or reverse primer name indicates the gene region of bacterial genome to which the primer hybridizes relative to a reference sequence eg: the forward primer name 16S_EC_1077_1106 indicates that the primer hybridizes to residues 1077-1106 of the gene encoding 16S ribosomal RNA in an *E. coli* reference sequence represented by a sequence extraction of coordinates 4033120..4034661 from GenBank gi number 16127994 (as indicated in Table 2). As an additional example: the forward primer name BONTA_X52066_450_473 indicates that the primer hybridizes to residues 450-473 of the gene encoding *Clostridium botulinum* neurotoxin type A (BoNT/A) represented by GenBank Accession No. X52066 (primer pair name codes appearing in Table 1 are defined in Table 2). In Table 1, U^a = 5-propynyluracil; C^a = 5-propynylcytosine; * = phosphorothioate linkage. The primer pair number is an in-house database index number.

Table 1: Primer Pairs for Identification of Bacterial Bioagents

Primer pair number	For. primer name	Forward sequence	For. SEQ ID NO:	Rev. primer name	Reverse sequence	Rev. SEQ ID NO:
1	16S_EC_107	GTGAGATGTTGGGTTAA	1	16S_EC_1175	GACGTCATCCCACTTCC	368

	7 1106 F	GTCCCGTAACGAG		1195 R	TC	
266	168 EC 108 2 1100 F	ATGTTGGGTTAAGTCC C	2	168 EC 1177 1196 106 1 16 R	TGACGTCATGGCCACCTTC	372
265	168 EC 108 2 1100 F	ATGTTGGGTTAAGTCC C	2	168 EC 1177 1196 106 R	TGACGTCATGGCCACCTTC	373
230	168 EC 108 2 1100 F	ATGTTGGGTTAAGTCC C	2	168 EC 1177 1196 F	TGACGTCATGGCCACCTTC	374
263	168 EC 108 2 1100 F	ATGTTGGGTTAAGTCC C	2	168 EC 1525 1541 R	AAGGAGGTGATCCAGCC	382
2	168 EC 108 2 1106 F	ATGTTGGGTTAAGTCC C	3	168 EC 1175 1197 R	TTGACGTCATGGCCACCTTC	371
278	168 EC 109 0 1111 2 F	TTAAGTCCCGCAACGAG	4	168 EC 1175 1196 R	TGACGTCATGGCCACCTTC	369
361	168 EC 109 0 1111 2 T	TTTAAAGTCCCGCAACGAG	5	168 EC 1175 1196 T	TTGACGTCATGGCCACCTTC	370
3	168 EC 109 0 1111 F	TTAAGTCCCGCAACGAG	6	168 EC 1175 1196 F	TGACGTCATGGCCACCTTC	369
256	168 EC 109 2 1109 F	TAGTCCCGCAACGAGC	7	168 EC 1174 1195 R	GACGTCATGGCCACCTTC	367
159	168 EC 110 0 1116 F	CAACGAGCGCAACCTTC	8	168 EC 1174 1189 R	TCCCACTTCCTCC	366
247	168 EC 119 5 1213 F	CAAGTCATCATGGCCCTTC	9	168 EC 1525 1541 R	AAGGAGGTGATCCAGCC	382
4	168 EC 122 2 1241 F	GCTACACACGTGTACAC	10	168 EC 1303 1323 R	CGAGTTGACGATCGGATC	376
232	168 EC 130 3 1323 F	CGGATTTGAGTCTGCAAC	11	168 EC 1389 1407 R	GACGCGCGGTGTGTACAA	378
5	168 EC 133 2 1353 F	AAGTCCGAATCGTAGT	12	168 EC 1389 1407 R	GACGCGCGGTGTGTACAA	378
252	168 EC 136 7 1387 F	TACGCTGAATACGTTCC	13	168 EC 1485 1506 R	ACCTTGTACGACTTACCC	379
250	168 EC 138 7 1407 F	GCCTTGTACACACCTTC	14	168 EC 1494 1513 R	CACGGCTACCTTGTACGA	381
231	168 EC 138 9 1407 F	CTTGTACACACCGCCCG	15	168 EC 1525 1541 R	AAGGAGGTGATCCAGCC	382
251	168 EC 139 0 1411 F	TTTACACACCGCCCGT	16	168 EC 1486 1505 R	CCTTGTACGACTTACCC	380
6	168 EC 30 54 F	TGAACGCTGGTGGCATG	17	168 EC 105 126 R	TACGATTACTACCGGTC	361
243	168 EC 314 332 F	CACCTGGAACTGAGACAC	18	168 EC 556 575 R	CTTTACGCCGATTAATTC	385
7	168 EC 38 64 F	GTGGCATGCTCAATACAC	19	168 EC 101 120 R	TTACTACCGCTCGCGCG	357
279	168 EC 405 432 F	TGAGTGATGAAGCCTTC	20	168 EC 507 527 R	CGGCTGTGCGACGAATTC	384
8	168 EC 49 69 F	TACACATGCAAGTCGA	21	168 EC 104 120 R	TTACTACCGCTCGCGCG	359
275	168 EC 49 68 F	TACACATGCAAGTCGA	21	168 EC 1061 1079 R	ACGACACGAGTCGACGAC	364
274	168 EC 49 68 F	TACACATGCAAGTCGA	21	168 EC 880 894 R	CGTACTCCCCAGGGG	390
244	168 EC 518 536 F	CCAGCAGCGCGGTAAT	22	168 EC 774 795 R	GTATCTAATCTGTTTGCT	387
226	168 EC 556 575 F	CGGAATTACTGGGCGTAA	23	168 EC 683 700 R	CGCATTTACCGCTACAC	386
264	168 EC 586 575 F	CGGAATTACTGGGCGTAA	23	168 EC 774 795 R	GTATCTAATCTGTTTGCT	387
273	168 EC 586 700 F	GTGTAGCGGTGAAATGC	24	168 EC 1303 1323 R	CGAGTTGACGATCGGATC	377
9	168 EC 683 700 F	GTGTAGCGGTGAAATGC	24	168 EC 774 795 R	GTATCTAATCTGTTTGCT	387
158	168 EC 683 700 F	GTGTAGCGGTGAAATGC	24	168 EC 880 894 R	CGTACTCCCCAGGGG	390
245	168 EC 7 3 F	GAGAGTTTATCTCTGGC	25	168 EC 967 985 R	GGAAGGTTCTTCGCGTTC	396
294	168 EC 713 732 F	AGAAACCGATGCGGA	25	168 EC 101 122 R	TGTACTACCGCGCTGCGC	358
10	168 EC 713 732 T	AGAAACCGATGCGGA	26	168 EC 789 809 R	CGTGGACTACAGGGTATC	388
346	168 EC 713 732 T	TAGAACCGATGCGGA	27	168 EC 789 809 T	TCGTGGACTACAGGGTATC	389
228	168 EC 774	GGGAGCAACAGGATTA	28	168 EC 880	CGTACTCCCCAGGGG	390

	795 F	GATAC		894 R	
11	168 EC 785 806 F	GGATTAGAGACCTGGT AGTCC	29	168 EC 880 897 R	GGCCGTACTCCCCAGGCG
347	168 EC 785 806 TMO F	TGGATTAGAGACCTGG TAGTCC	30	168 EC 880 897 TMO R	TGGCCGTACTCCCCAGGCG
12	168 EC 785 810 F	GGATTAGATACCTGGT AGTCCAGC	31	168 EC 880 897 2 R	GGCCGTACTCCCCAGGCG
13	168 EC 789 810 F	TAGATACCTGGTAGTC CAGCG	32	168 EC 880 894 R	CGTACTCCCGAGGCG
255	168 EC 789 810 F	TAGATACCTGGTAGTC CAGCG	32	168 EC 882 899 R	GGACCGTACTCCCCAGG
254	168 EC 791 812 F	GATACCTGGTAGTCCA CAGCG	33	168 EC 886 904 R	GCTTTCGCGAGCTATCCC
248	168 EC 8 2 7 F	AGAGTTTGTATCATGGCT CAG	34	168 EC 1525 1541 R	AMGAGGTGATCCAGCC
242	168 EC 8 2 7 F	AGAGTTTGTATCATGGCT CAG	34	168 EC 342 359 R	ACTGCTGCGCTCCCGTAG
253	168 EC 804 822 F	ACACGCGCGTAAACGAT G	35	168 EC 909 929 R	CCCCCGTCAATTCCTTGA GT
246	168 EC 937 954 F	AAGCGGTGGAGCATGTG G	36	168 EC 1220 1240 R	ATTGTAGCAGGTGTAGTAC CC
14	168 EC 960 981 F	TTTCGATGCAACGCGAG AACCT	37	168 EC 1054 1073 R	ACGAGCTGACGACGCCAT G
348	168 EC 960 981 TMO F	TTTCGATGCAACGCGAA GAACTT	38	168 EC 1054 1073 TMO R	TACGAGCTGACGACGCCA TG
119	168 EC 969 985 1P F	ACGCGAGAGAACCTTA TTC	39	168 EC 1061 1078 2P R	ACGACACGAGTCCGACGAC
115	168 EC 969 985 F	ACGCGAGAGAACCTTACC	39	168 EC 1061 1078 R	ACGACACGAGCTGACGAC
272	168 EC 969 985 F	ACGCGAGAGAACCTTACC	40	168 EC 1389 1407 R	GACGGCGGTGTGTACAG
344	168 EC 971 990 F	GCGAGAGAACCTTACCAG GTC	41	168 EC 1043 1062 R	ACAACCATGACCACTGT C
120	168 EC 972 985 2F F	CGAAGAAUUTTTAC	42	168 EC 1064 1078 2P R	ACACGAGTCCGAC
121	168 EC 972 985 F	CGAAGAACCTTACC	42	168 EC 1064 1075 R	ACACGAGCTGAC
1073	238 BRM 117 10 1129 F	TGCGGGAAGATGTATAC GGG	43	238 BRM 117 6 1201 R	TGCGGAGCTTACGAGACGC TCTCCTA
1074	238 BRM 51 5 536 F	TGCGGGAAGATGTATAC AGCCT	44	238 BRM 616 635 R	TGCGGAGCTGCTTTCGTAC G
241	238 BS - 68 -44 F	AACTAGATAACAGTAG ACATCAC	45	238 BS 5_21 R	GTGCGCCCTTTTCACTT
235	238 EC 160 2 1620 F	TACCCCAAAACGACACA GG	46	238 EC 1686 1703 R	CCTTCTCCGAGTAGC
236	238 EC 168 5 1703 F	CCGTAACTTCGGGAGAA GG	47	238 EC 1828 1842 R	CACCGGGCAGGCTC
16	238 EC 182 6 1843 F	CTGACACTGCCCGGTG C	48	238 EC 1906 1924 R	GACCGTTATAGTAAAGGCC
349	238 EC 182 6 1843 TMO D F	TCTGACACTGCCCGGT GC	49	238 EC 1906 1924 TMO R	TGACCGTTATAGTAAAGGCC C
237	238 EC 182 7 1843 F	GACGCTGCGCGGTGC	50	238 EC 1929 1949 R	CCGACAGGAATTCGCTA CC
249	238 EC 183 1 1849 F	ACCTGCCAGTGTGGA AG	51	238 EC 1919 1936 R	TGCGTACCTTAGGACCGT
234	238 EC 187 207 F	GGGAACTGAACATCTTA AGTA	52	238 EC 242 256 R	TTTCGCTGCGCGTAC
233	238 EC 23 37 F	GGTGGATGCTTTGGC	53	238 EC 115 130 R	GGGTTTCCCATTCGG
238	238 EC 243 4 2456 F	TAAGTACTCCGGGATA ACAGGC	54	238 EC 2490 2511 R	AGCCGACATCGAGTGCCA AAC
257	238 EC 258 6 2607 F	TAGAAGCTCGCGAGCA GTTCG	55	238 EC 2658 2677 R	AGTCATCCCGGTCTCTTC G
239	238 EC 259 9 2616 F	GACAGTTTCGGTCCCTAT G	56	238 EC 2653 2669 R	CCGGTCTCTCTGACTA
18	238 EC 264 5 2669 2 F	CTGTCCCTAGTACGAGA GGAACGG	57	238 EC 2751 2767 R	GTTCGTCTAGATGCTT TCAGC
17	238 EC 264 5 2669 F	TCTGTCCCTAGTACGAG AGGACCGG	58	238 EC 2744 2761 R	TGCTTAGATGCTTTACAG
118	238 EC 264 6 2667 F	CTGTCTTAGTACGAGA GGAAC	59	238 EC 2745 2765 R	TTTCGTCTAGATGCTT AG
360	238 EC 264	TCTGTCTTAGTACGAG	60	238 EC 2745	TTTCGTCTAGATGCTT

	6_2667_TMO D F	AGGACC		2765_TMOD R	CAG	
147	238 EC 265 2 2669 F	CTAGTACGAGAGACCG	61	238 EC 2741 2760 R	ACTTAGATGCTTCAGCGG	413
240	238 EC 265 3 2669 F	TGCTACGAGAGACCGG	62	238 EC 2737 2759 R	TTAGATGCTTCAGCACTT	412
20	238 EC 493 518 2 F	GCGAGGTGAAGAGATC	63	238 EC 551 571 2 R	ACAAAAGGCACGCCATCAC	418
19	238 EC 493 518 F	GGGGAGTGAAGAGATC	63	238 EC 551 571 R	ACAAAAGGTACGCCGTAC	419
21	238 EC 971 992 F	CGAGAGGGAACACCC	64	238 EC 1059 1077 R	TGGCTGCTTCAAGCCAAC	400
1158	AB_MLST- 11- OIF007_120 2 1225 F	TCGTGCCCGCAATTTCG	65	AB_MLST-11- OIF007_1266 1296 R	TAATGCCGGTAGTGCAAT	420
1159	AB_MLST- 11- OIF007_120 2 1225 F	TCGTGCCCGCAATTTCG	65	AB_MLST-11- OIF007_1299 1316 R	TGCACCTGCGGTGAGG	421
1160	AB_MLST- 11- OIF007_123 4 1264 F	TTGTAGCACGCAAGGC	66	AB_MLST-11- OIF007_1335 1362 R	TGCCATCCATAATCACGCC	422
1161	AB_MLST- 11- OIF007_132 7 1356 F	TAGGTTTACGTGATAT	67	AB_MLST-11- OIF007_1422 1448 R	TGCCAGTTTCCACATTCA	423
1162	AB_MLST- 11- OIF007_134 5 1369 F	TCGTGATTATGGATGCG	68	AB_MLST-11- OIF007_1470 1494 R	TGCGTTGAGTGATGATG	424
1163	AB_MLST- 11- OIF007_135 1 1375 F	TTATGATGGCAACGTC	69	AB_MLST-11- OIF007_1470 1494 R	TGCGTTGAGTGATGATG	424
1164	AB_MLST- 11- OIF007_138 7 1412 F	TCCTTGCCATTGAAGAT	70	AB_MLST-11- OIF007_1470 1494 R	TGCGTTGAGTGATGATG	424
1165	AB_MLST- 11- OIF007_154 2 1569 F	TACTAGCGGTAAAGCTTA	71	AB_MLST-11- OIF007_1656 1680 R	TGAGTCGGGTTCACTTTAC	425
1166	AB_MLST- 11- OIF007_156 6 1593 F	TTGCCAATGATATTCGT	72	AB_MLST-11- OIF007_1656 1680 R	TGAGTCGGGTTCACTTTAC	425
1167	AB_MLST- 11- OIF007_161 1 1638 F	TCGGCGAAATCGCTATT	73	AB_MLST-11- OIF007_1731 1757 R	TACCGGAAGCACCAGGAC	427
1168	AB_MLST- 11- OIF007_172 6 1752 F	TACCACATTATATTCGT	74	AB_MLST-11- OIF007_1790 1821 R	TGCAACTGAATGAGTTGCA	428
1169	AB_MLST- 11- OIF007_179 2 1826 F	TTATACTTACTGCAAT	75	AB_MLST-11- OIF007_1876 1909 R	TGAATTATGCAAGAGTGA	429
1170	AB_MLST- 11- OIF007_179 2 1826 F	TTATACTTACTGCAAT	75	AB_MLST-11- OIF007_1895 1927 R	TGCCGTAACATACATAGA	430
1152	AB_MLST- 11- OIF007_185 214 F	TATTGTTTCAATGTAC	76	AB_MLST-11- OIF007_291 324 R	TCACAGGTTTCACTTCATC	432
1171	AB_MLST- 11- OIF007_197 0 2002 F	TGGTTATGTACCAATA	77	AB_MLST-11- OIF007_2097 2118 R	TGACGCGATCGATACCAAC	431
1154	AB_MLST- 11- OIF007_206 239 F	TGAAGTCGCTGATGATA	78	AB_MLST-11- OIF007_318 344 R	TCCGCCAAAACCTCCOCTT	433

1153	AB MLST-11- OIF007_260 289 F	TGGAACGTTATCAGGTG CCCCAAAATTCG	79	AB MLST-11- OIF007_364 393 R	T'TGCAATCGACATATCCAT T'TCACCATGCC	434
1155	AB MLST-11- OIF007_522 552 F	TCGGTTTAGTAAAGAA CGTATTGCTCAACC	80	AB MLST-11- OIF007_587 610 R	T'TCTGCTTGAGGAATAGTG C GTGG	435
1156	AB MLST-11- OIF007_547 571 F	TCACCTGACTGCGTGA ATGGTTGT	81	AB MLST-11- OIF007_656 686 R	T'ACGTTCTACGATTCTTC A'TCAGGTACATC	436
1157	AB MLST-11- OIF007_601 627 F	TCARGCAGAGCTTTGG AAGAAGAAGG	82	AB MLST-11- OIF007_710 736 R	T'ACAACCTGTATAAACACGA C CAGAAGC	437
1151	AB MLST-11- OIF007_62 91 F	TGAGATTGCTGAACATT TAATGCTGATTGA	83	AB MLST-11- OIF007_169 203 R	T'TGTACATTTGAACAAATA T'GCATGACATGTGAAT	426
1100	ASD_FRT_1 29 F	TTGCTTAAAGTTGGTTT TATTGGTTGGCG	84	ASD_FRT_86 116 R	T'GAGATGTGCAAAAACAG T'TGGCAAAATAC	439
1101	ASD_FRT_43 76 F	TCAGTTTAAATGTCTCG TAGTATCGAATCAAAAG	85	ASD_FRT_129 155 R	T'CCATATTGTTGCTGATAAAA C CTGTTGGC	438
291	ASB_EG_40 5 427 F	GCACAACTGCGGCGTCG G	86	ASB_EG_521 538 R	A'CGCCACGAGGTAGTCGC	440
485	BONTA_X520 66_450_473 F	TCTAGTAATAATAGGAC CCTCAGC	87	BONTA_X5206 6_517_539 R	T'AACCATTTGCGCTTAGAT T'CAA	441
486	BONTA_X520 66_450_473 F F	T*U*C*AGTAATAATAG GA*U*U*U*C*U*U*G C	87	BONTA_X5206 6_517_539P R	T'AACCA*C*U*C*U*U*G GTAAGA*C*U*U*AA	441
481	BONTA_X520 66_538_552 F	TATGGCTCTACTCAA	88	BONTA_X5206 6_647_660 R	T'GTACTGCTGGAT	443
482	BONTA_X520 66_538_552 F F	TA*C*GGC*C*U*U*C*U *U*C*U*U*AA	88	BONTA_X5206 6_647_660P R	T'G*C*U*U*U*U*U*U*U*U*U *GGAT	443
487	BONTA_X520 66_591_620 F	TGAGTCACCTTGAAGTIG ATACRAATCCTCT	89	BONTA_X5206 6_644_671 R	T'CATGTGCTAATGTACTCG C'TGGATCTG	442
483	BONTA_X520 66_701_720 F	GAATAGCAATTAATCCA AAT	90	BONTA_X5206 6_759_775 R	T'TACTTCTAACCCACTC	444
484	BONTA_X520 66_701_720 F F	GAA*C*AG*U*AA*C*U *AA*C*U*U*AAAT	90	BONTA_X5206 6_759_775P R	T'TA*U*U*U*U*U*U*U*U*U U*U*U*U*U*U*U*U*U	444
774	CAF1_AF053 947_33407 33430 F	TCAGTTCGGTTATCGCC ATTGCAT	91	CAF1_AF0539 47_33494_33 514 R	T'CGCGGCTGGTTCAACAG AG	445
776	CAF1_AF053 947_33435 33447 F	TGGAACATTGCAACTG CTAATG	92	CAF1_AF0539 47_33499_33 517 R	T'GATGCGGCTGGTTCAAC	446
775	CAF1_AF053 947_33515 33541 F	TCACCTTTCATATTAAG GAAGGCGCTC	93	CAF1_AF0539 47_33595_33 621 R	T'CCGTGTTTATAGCGGCCA AAGTAGA	447
777	CAF1_AF053 947_33687 33716 F	TCAGGATGGAATAAC ACCAATTCACTAC	94	CAF1_AF0539 47_33755_33 782 R	T'CAAGCTTCTCACCGTTTA CCTTAGGAG	448
22	CAPC_BA_10 4 131 F	GTTATTATGACACTGGT TTTATCAGCC	95	CAPC_BA_180 205 R	T'GAATCTTGAACACCATC C GTAAG	449
23	CAPC_BA_11 4 133 F	ACTCGGTTTAAKACAG CCG	96	CAPC_BA_185 205 R	T'GAATCTTGAACACCATC C G	450
24	CAPC_BA_27 4 303 F	GATTATTGTTATCTGT TATGCCATTTGAG	97	CAPC_BA_349 376 R	GTAACCCCTGCTCTTGAAT T'GTATTTGC	451
350	CAPC_BA_27 4_303_TMOD F	TGATTATTGTTATCTGT TTATGCCATTTGAG	98	CAPC_BA_349 376_TMOD R	T'GTAAACCCCTGCTCTTGA T'TGTNTTTC	452
25	CAPC_BA_27 6 296 F	TTATGTTATCTCGTTA TGCC	99	CAPC_BA_358 377 R	GGTAAACCCCTGCTCTTGA T'	453
26	CAPC_BA_28 1 339 F	GTTATCTGTTATGCCA TTG	100	CAPC_BA_361 378 R	T'GGTAACCCCTGCTCTTGA T'	454
27	CAPC_BA_31 5 334 F	CCCTGGTATTGGAGTTA TTG	101	CAPC_BA_361 378 R	T'GGTAACCCCTGCTCTTGA T'	454
1053	CJST CJ_10	TTGAGGGTATGCMCGT	102	CJST CJ_116	T'CCCTCATGT'TTAAATGA	456

	80 1110 F	CTTTTGTATTCTTT		6 1198 R	TCAGGATAAAAAGC	
1063	CJST_CJ_12 68 1299 F	AGTTATAAACACGGCTT TCTATGGCTTATCC	103	CJST_CJ_134 9 1379 R	TCGGTTTAAAGCTTACATG ATCGTAAGGATA	457
1050	CJST_CJ_12 90 1320 F	TGCTTATCCAAATTTA GATCGTGGTTTATC	104	CJST_CJ_140 6 1433 R	TTTGCTCATGATCGCATG AAGCATAAA	458
1058	CJST_CJ_16 43 1670 F	TTATCGTTTGTGGAGCT AGTGTCTATGC	105	CJST_CJ_172 4 1752 R	TCGAATGTGTGCTATG TCA GCAAAAGAT	459
1045	CJST_CJ_16 68 1700 F	TGCTCGAGTATGACT TTCTTAATTTAGAGA	106	CJST_CJ_177 4 1799 R	TGAGCTGTGGAAGAG GAC TTGAGTG	460
1064	CJST_CJ_16 80 1713 F	TGATTTTGTCAAAATTTA GAGAAATTCGGAGTAA	107	CJST_CJ_179 5 1822 R	TATGTGTAGTGTAGCT TAC TACATGAGC	461
1056	CJST_CJ_18 80 1910 F	TCCCAATTAATCTGCC ATTITTCAGGTAT	108	CJST_CJ_198 1 2011 R	TGGTCTTACTGTCTT TGC ATAAACTTTCCA	462
1054	CJST_CJ_20 60 2090 F	TCCCGGACTTAATATCA ATGAAATTTGGGA	109	CJST_CJ_214 8 2174 R	TGATCGCATCAACCA TCA AAGCAAA	463
1059	CJST_CJ_21 65 2194 F	TGGCGATCGTTTGGTGG TTGTGATGTAA	110	CJST_CJ_224 7 2278 R	TCCACACTGGATTTGA ATT TACCTTGTGTTT	464
1046	CJST_CJ_21 71 2297 F	TGCTTGGTGGTGGTGG ATGAAAGG	111	CJST_CJ_228 3 2313 R	TGCTTTCAAGACCC ATT GCTCATATAGT	465
1057	CJST_CJ_21 85 2212 F	TAGATGAAGAGGCGAA GTGGCTAATGG	112	CJST_CJ_228 3 2316 R	TGAATTTCTTCAAGC ACC ATTGCTCATATAGT	466
1049	CJST_CJ_26 36 2668 F	TGCTTAGAAGATCTTAA AAATTTCCGCAACTT	113	CJST_CJ_275 3 2777 R	TTGCTGCCATGCAAA GCC TACAGC	467
1062	CJST_CJ_26 78 2703 F	TCCCGAGGACCCCTGA AATTTCAAC	114	CJST_CJ_276 0 2787 R	TGTGCTTTTTTGTGCTG CCA TAGCAAGC	468
1065	CJST_CJ_28 57 2887 F	TGCTATTCTTATGAAG CTGTGTTCTTAGCA	115	CJST_CJ_296 5 2998 R	TGCTTCAAAAGCATTT TTT ACATTTTCTGTAAG	469
1055	CJST_CJ_28 69 2895 F	TGAAGCTTGTCTTTAG CAGACTCA	116	CJST_CJ_297 9 3007 R	TCTCTCTGTGCTCAAAA GCGATTTTA	470
1051	CJST_CJ_32 67 3293 F	TTTGATTTTACGCGCTC CTCCAGTGC	117	CJST_CJ_335 6 3385 R	TCAAAGACCGCGAC TAA TTCATCATTTA	471
1061	CJST_CJ_36 0 393 F	TCTCTGTTATCCCTGAAG TAGTATATCAAGTTTGT T	118	CJST_CJ_443 477 R	TACAACCTGGTTCAAAACA TTAAGCTGTAATGTG	473
1048	CJST_CJ_36 0 394 F	TCTCTGTTATCCCTGAAG TAGTATATCAAGTTTGT T	119	CJST_CJ_442 476 R	TCAACTGGTTCAAAACA CAT TAAGTTGTAAATGTG	472
1052	CJST_CJ_5 39 F	TAGGCGAAGATATACAA AGATTTATAGAGCTAG A	120	CJST_CJ_104 137 R	TCCCTTATTTTCTTTT CTA CTACCTTCGGATAT	455
1047	CJST_CJ_58 4 616 F	TCCAGGCAAAATGTATG AAAAATGTCCCAAGAG	121	CJST_CJ_663 692 R	TTCAATTTCTGCTCCA AAG TAAGCAGTATC	474
1060	CJST_CJ_59 9 632 F	TGA AAAATGTCCCAAGAA GCATAGCAAAAAGGCA	122	CJST_CJ_711 743 R	TCCCGACAAATGAGTT GTA TCAACTATTTTTC	475
1096	CTXA_VBC_1 17 142 F	TCTTATGCGCAAGAGGAC AGAGTGAAGT	123	CTXA_VBC_19 4 218 R	TGCTTACAAATCCCG TGT GAGTTC	476
1097	CTXA_VBC_3 51 377 F	TGTATTAGGGGACATACA GTCTCTATCC	124	CTXA_VBC_44 1 465 R	TGTCTATCAAGCACCC AAA ATGAAC	477
28	CYA_BA_105 5 1072 F	GAAAGAGTTCGGATTGG G	125	CYA_BA_1112 1130 R	TGTTGACCATGCTTCT TAG 1130 R	479
277	CYA_BA_134 9 1370 F	ACACGGAAGTACAATAC AAGAC	126	CYA_BA_1426 1447 R	GTCTACATTTTATGAC CAT CAC	480
30	CYA_BA_135 3 1379 F	CGAAGTACAATACAAAG CAAAAGAGG	127	CYA_BA_1448 1467 R	TGTTAAGCGGCTTCAAG ACC 1467 TMOO	482
351	CYA_BA_135 3 1379 F	TGGAAGTACAATACAAAG ACAAAAGAGG	128	CYA_BA_1448 1467 TMOO R	TTGTTAACGGCTTCAA GAC CC	483
31	CYA_BA_135 9 1379 F	ACAAATAGAGCAAAAG AGG	129	CYA_BA_1447 1461 R	CGGCTTCAAGACGCC	481
32	CYA_BA_914 937 F	CAGGCTTAGTACCAGAA CATGCAG	130	CYA_BA_999 1025 R	ACCACCTTTTATAGG TTT GTAGCTAC	484
33	CYA_BA_916 935 F	GGTTTAGTACCAGAAACA TGC	131	CYA_BA_1003 1025 R	CCACTTTTATATAGGT TTT TAGC	478
115	DNAX_EC_42 8 449 F	CGCGGTACTTCAACGAC AGCCA	132	DNAX_EC_503 522 R	CGCGGTGCGCTGTGATG A 522 R	485
1102	GALE_FRT_1 68 199 F	TTATCAGCTAGACCTTT TGTAAAGCTTAAGC	133	GALE_FRT_24 1 269 R	TCACCTACAGCTTTAA AGC CAGCAAAATG	486
1104	GALE_FRT_3 9 339 F	TCCAGGTCACTTAATC TTACTTCACTTAATC	134	GALE_FRT_39 0 422 R	TCTTCTGAAGGGGTG GTT TATATTCATCCA	487
1103	GALE_FRT_8 34 865 F	TCAAAAGGCTTCAAGTCA AAGAGTTCATATC	135	GALE_FRT_90 1 925 R	TGAGCTTGGCAATCAT AGC AAACT	488
1092	GLTA_RKP_1 023 1055 F	TCGCTTCTTACAANTAG CAATGAACTTGAAGC	136	GLTA_RKP_11 29 1156 R	TTGGCGACGCTATACC CAT AGCTTTATA	489
1093	GLTA_RKP_1 043 1072 F	TGGAGCTTTGAAGCTATC GCTCTTAAAGATG	137	GLTA_RKP_11 38 1162 R	TGAACATTTGAGGCGTAT ACCCAT	490

	GLTA_RKP_1 043_1072_3 F	TGGAACTTGAAGCTCTC GCTCTTAAAGATG		GLTA_RKP_11 38_1164_R	TGTGAACATTTCGGACGGT ATACCCAT	
1094			138			492
	GLTA_RKP_1 043_1072_F	TGGGACTTGAAGCTATC GCTCTTAAAGATG		GLTA_RKP_11 38_1162_R	TGACATTTCGGACGGTAT ACCCAT	491
1090			139			
	GLTA_RKP_4 CO_428_F	TCTCTGCAACCTATGGC TATTATGCTTGG		GLTA_RKP_49 9_529_R	TGCTGGGATCTTACCAAT CATTTCTAATAGC	493
1091			140			
	GLTA_RKP_4 CO_428_F	TCTTCTCATCTATGGC TATTATGCTTGG		GLTA_RKP_50 5_534_R	TGCGATGGTAGGTA/CTTA GCAATCAITCT	494
1095			140			
	GROL_EC_21 9_242_F	GGTGAAGAAGTTGGCT CTAAAGC		GROL_EC_328 350_R	TTGAGGTCCATCGGGTTCA TGCC	496
224			141			
	GROL_EC_49 6_518_F	ATGGACAAGGTTGGCAA GGAAGC		GROL_EC_577 596_R	TAGCGCGGTGCAATTCGA T	498
280			142			
	GROL_EC_51 1_536_F	AAGGAAGGCTGATCAC CGTTGAGA		GROL_EC_571 593_R	CCGCGGTGCAATTCGATGC CTTC	497
281			143			
	GROL_EC_94 1_959_F	TGGAAGATCTGGGTGAG GC		GROL_EC_103 9_1060_R	CACTCTGCTGACGGATCTG AGC	495
220			144			
	GYRA_AFI100 557_4_23_F	TCTGCCCGTGTGCTTGG TGA		GYRA_AFI005 57_119_142_R	TGCAACCGAAGTTACCTTG ACCAT	499
924			145			
	GYRA_AFI100 557_70_94_F	TCCATTGTGCTATGCT TCAAGACT		GYRA_AFI005 57_178_201_R	TGCCAGCTTAGTCAACGG ACTTC	500
925			146			
	GYRB_AB008 700_19_40_F	TCAGGTGGCTTACACGG CGTAG		GYRB_AB0087 00_111_140_R	TATTGGGATACCATGAT GATATTCTTG	501
926			147			
	GYRB_AB008 700_265_29_F	TCTTCTTGGAATGCTGG TGACGTATG		GYRB_AB0087 00_369_395_R	TGCTTGAGATGGTTTATC CTCTGTTG	502
927			148			
	GYRB_AB008 700_368_39_F	TCAACGAAGGTAAAC CATCTCAACG		GYRB_AB0087 00_466_494_R	TTTGTGAACACGCAACAT TTTCTTGGA	503
928			149			
	GYRB_AB008 700_477_50_F	TGTTGCTGTTTTCACAA ACAACTTCCA		GYRB_AB0087 00_611_632_R	TCACGCGCATCATCACCG TCA	504
929			150			
	GYRB_AB008 700_760_78_F	TACTTACTTGAGAATCC ACAAGCTGCAA		GYRB_AB0087 00_862_888_R	TCTTGCAATATCTAATGCA CTCTTAGC	505
949			151			
	GYRB_AB008 700_760_78_F	TACTTACTTGAGAATCC ACAAGCTGCAA		GYRB_AB0087 00_862_888_R	ACCTGCAATATCTAATGCA CTCTTAGC	506
930			151			
	HFLB_EC_10 82_1102_F	TGGCGAACCTGGTGAAC GAAGC		HFLB_EC_114 4_1168_R	CTTTGCGTTTCTGCACTC AACCAT	507
222			152			
	HUPB_CJ_11 3_134_F	TAGTTGCTCAACAGCT GGCTC		HUPB_CJ_157 2_188_R	TCCTTAATAGTAGAATAA CTGCATCAGTAGC	509
1128			153			
	HUPB_CJ_76 102_F	TCCCGGAGCTTTTATGA CTAAAGCAGAT		HUPB_CJ_114 1_135_R	TAGCCAGCTGTTTGAGCA ACT	508
1130			154			
	HUPB_CJ_76 102_F	TCCCGGAGCTTTTATGA CTAAAGCAGAT		HUPB_CJ_157 2_188_R	TCCTTAATAGTAGAATAA CTGCATCAGTAGC	510
1129			154			
	ICD_CXB_17 6_198_F	TGCGCTGGGAAAAATCC TAGCTG		ICD_CXB_224 2_247_R	TAGCCCTTTCTCGGCGGTA GATCT	512
1079			155			
	ICD_CXB_92 120_F	TTCTGACCCAGCCCAAT ATTCCCTTTATC		ICD_CXB_172 1_194_R	TAGGATTTTTCACGCGGG CATC	510
1078			156			
	ICD_CXB_93 120_F	TCTTGACCCAGCCCAAT TCTCTTATC		ICD_CXB_172 2_194_R	TAGGATTTTTCACGCGGG CATC	511
1077			157			
	INFB_EC_11 03_1124_F	CTGCTGAAAACGAGCTG GAAGA		INFB_EC_117 4_1191_R	CATGAAGTCAACACCGG T	513
221			158			
	INFB_EC_13 47_1367_F	TGCGTTTACCGCAATGC GTGC		INFB_EC_141 4_1432_R	TGCGCATCACGCGGTGCTC T	514
964			159			
	INFB_EC_13 65_1393_F	TGCTCGTGGTGACACAG TAACGGATATTA		INFB_EC_143 9_1467_R	TGCTGCTTTGCGATGGTGA ATGCTTCAA	515
34			160			
	INFB_EC_13 65_1393_TM OD_F	TTGCTGCTGGTGACAA GTAAAGGATATTA		INFB_EC_143 9_1467_TMDD R	TTGCTGCTTTGCGATGGT AATGCTTCAA	516
352			161			
	INFB_EC_19 69_1994_F	CGTCAGAGGTAAATTCG TGAAGTTAA		INFB_EC_203 8_2058_R	AATCTGCGCTTGGCTGATG TT	517
223			162			
	INV_U22457 _1558_1581_F	TGTTAAACAGAGCCTTAT AGGCGCA		INV_U22457 1615_1643_R	TTGCGTTCAGATTAATCTT TACCAA	518
781			163			
	INV_U22457 515_539_F	TGCTCTCTTGGTATGAC TCTGCTTC		INV_U22457 571_598_R	TGTTAAGTGTGTCGGGCT GCTCTTAT	519
778			164			
	INV_U22457 699_724_F	TGCTGAGGCGCTGGACG ATTATTTAT		INV_U22457 753_776_R	TCACGCGAGCATGCCATC CATTC	520
779			165			
	INV_U22457 834_858_F	TTATTTACTCTGCATCC CACACTG		INV_U22457 942_966_R	TGACCCAAAGCTGAAAGCT TTATCTG	521
780			166			

1106	IPAH_SGF_1 13_134_F	TCCTTGACGCGCTTCC GATAC	167	IPAH_SGF_17 2_191_R	TTTTCCAGCCATCGACGGA C	522
1105	IPAH_SGF_2 58_277_F	TGAGGACCGCTGTCGCGC TCA	168	IPAH_SGF_30 1_327_R	TCCTTCTGATGCGCTATGG ACCAAGGAG	523
1107	IPAH_SGF_4 62_486_F	TCAGACCAATGCTCGCAG AGAACTT	169	IPAH_SGF_52 2_540_R	TGTCACCTCCGACACGCCA	524
1080	IS1111A_NC 002971_686 6_6891_F	TCAGTATGATCCACCG TAGCCAGTC	170	IS1111A_NC 02971_6928_ 6954_R	TAAAGCTCGATACCAATG GTTCGCTC	525
1081	IS1111A_NC 002971_745 6_7483_F	TGGGTGACATTTCATCA TTTCATCGTTC	171	IS1111A_NC 02971_7529_ 7554_R	TCACACCACTCCTTATT CCCACTC	526
35	LEF_BA_103 3_1052_F	TCAGAAGAAAAAGAGC C	172	LEF_BA_1119 1_1135_R	GAATATCAATTGTGAGC C	527
36	LEF_BA_103 6_1066_F	CAAGAGAAAAAGAGCT TCTAAGACATATC	173	LEF_BA_1119 1_1159_R	AGATAAGATCAGBATA TCANTTGTAGC	528
37	LEF_BA_756 781_F	AGCTTTTGATATATATA TCGAGCCAC	174	LEF_BA_843_ 872_R	TCCTCCAGATAGATTTA TTCTTGTTCG	530
353	LEF_BA_756 781_THOD_F	TAGCTTTTGATATATAT ATCGAGCCAC	175	LEF_BA_843_ 872_THOD_R	TTCTTCCAGGATAGATTT ATTCTGTTCG	531
38	LEF_BA_758 778_F	CTTTTGATATATATATC GAGC	176	LEF_BA_843_ 865_R	AGGATAGATTTATTCTG TTGC	529
39	LEF_BA_795 815_F	TTTACAGCTTTATGCAC CG	177	LEF_BA_883_ 900_R	TCTTGACAGCATCCGTCG C	532
40	LEF_BA_883 899_F	CAACCGATGCTGGCAAG C	178	LEF_BA_939_ 958_R	CAGATAGAAATCGCTCCA G	533
782	LL_NC00314 3_236996 2367019_F	TGTAGCCGCTAAGCACT ACCATCC	179	LL_NC003143 2367073_23 67097_R	TCTCATCCGATATATACG CCATGA	534
783	LL_NC00314 3_2367172 2367194_F	TGGACGGCATCACGATT CTCTAC	180	LL_NC003143 2367249_23 67271_R	TGGCAACAGCTCAACACT TTGG	535
878	MECA_Y1405 1_3645_367 0_F	TGAAGTAGAATGACTG AAGTCCGA	181	MECA_Y14051 3690_3719 R	TGATCTGGAATGTTTATAT CTTTAAGGCTT	536
877	MECA_Y1405 1_3774_380 2_F	TAAACAACTAAGGTA ACATTGATCGCA	182	MECA_Y14051 3828_3854_ R	TCCCAATCTAATCTCCACA TACCATCT	537
879	MECA_Y1405 1_4507_453 0_F	TCAGGTACTGCTATCCA CCCTCAA	183	MECA_Y14051 4555_4581_ R	TGGATAGAAGTCAATGAA GGTGCTCT	538
880	MECA_Y1405 1_4510_453 0_F	TGTACTGCTATCCACCC TCAA	184	MECA_Y14051 4586_4610_ R	TATTCTTCGTTACTCATGC CATACA	539
882	MECA_Y1405 1_4520_453 0_F	TU ⁰ U ⁰ AD ⁰ U ⁰ C ⁰ U ⁰ AA	185	MECA_Y14051 4590_4600P R	C ⁰ AU ⁰ C ⁰ U ⁰ C ⁰ GU ⁰ UA	540
883	MECA_Y1405 1_4520_453 0_F	TU ⁰ U ⁰ AD ⁰ U ⁰ C ⁰ U ⁰ AA	185	MECA_Y14051 4600_4610P R	C ⁰ AC ⁰ C ⁰ U ⁰ C ⁰ U ⁰ GC ⁰ T	541
881	MECA_Y1405 1_4669_469 8_F	TCACCAAGTTCAACTCA AUAATATTATCA	186	MECA_Y14051 4765_4793_ R	TAAACCCCAAGATTTAT CTTTTGCCA	542
876	MECA_Y1405 51_3315_33 41_F	TTACACATATCGTAGC AATGAATCGA	187	MECA_Y1405 1_3367_3393 R	TGTGATATGGAGGTGAGA AGGTGTTA	543
914	OMPA_AY485 227_272_30 1_F	TTACTTCATTATGCTT GGTTACATTTCC	188	OMPA_AY4852 27_364_388 R	GAGCTGCGCCAAAGAAATA ATCGTC	544
916	OMPA_AY485 227_311_33 5_F	TACACAAATGAGGGGT AAGATGCG	189	OMPA_AY4852 27_424_453 R	TACGTCGCTTTAACTTGG TTATATTCAGC	545
915	OMPA_AY485 227_379_40 1_F	TGCGCAGCTCTTGSTAT CGAGTT	190	OMPA_AY4852 27_492_519_ R	TGCGGTGATCAGAAAGTTA CCGTGATT	546
917	OMPA_AY485 227_415_44 1_F	TGCGCTCGAGCTGAATA TAACCAAGTT	191	OMPA_AY4852 27_514_546_ R	TGCGGCTAGTTTTTNGTA ATTAAATCAGAAGT	547
918	OMPA_AY485 227_494_52 0_F	TCACGSGTAATCTTAT GTTACTTCG	192	OMPA_AY4852 27_569_596_ R	TGCTGCTATTTATAGTGAC CAGCGCTA	548
919	OMPA_AY485 227_551_57 7_F	TCAAGCGTACGTATTA TTAGGTGCTG	193	OMPA_AY4852 27_658_680_ R	TTTARGCGCCAGAAGCAC CAAC	550

920	OMPA AY485 227_555_58 1 F	TCCGTACGTATTATTAG GTGCTGGTCA	194	OMPA AY4852 227_635_662_ R	TCAACACCAGCGTTACCTA AAGTACCTT	549
921	OMPA AY485 227_556_58 3 F	TGCTACGTATTATTAG TGCTGGTCACT	195	OMPA AY4852 227_659_693_ R	TGCTTTAAGCGCAGAAAG CACCA	551
922	OMPA AY485 227_657_67 9 F	TGTTGGTGGCTTTCTGGC GCTTAA	196	OMPA AY4852 227_739_765_ R	TAAGCCAGCAAGAGCTGTA TAGTTCCA	552
923	OMPA AY485 227_660_68 3 F	TGGTGGCTTTCTGGCGCT TAAACGA	197	OMPA AY4852 227_786_807_ R	TACAGGAGCAGCAGGCTTC AAG	553
1089	OMPH RKP 1 192 1221 F	TCTACTGATTTTGGTAA TCTTCAGCACAG	198	OMPH RKP 12 68 1315 R	TAGCAGCAAAAGTTATCAC ACCTGCAT	554
1089	OMPH RKP 3 417 3440 F	TGCAAGTGGTACTTCAA CTAGGGG	199	OMPH RKP 35 20 3550 R	TGCTGTAGTTCTCTAGT TGTTCATTAA	555
1087	OMPH RKP 8 60 890 F	TTACAGGAAGTTTAGGT GGTATCTRAAAGG	200	OMPH RKP 97 2 996 R	TCTCTCAGCTTCTACCTGCT CCATTA	556
41	PAG BA 122 142 F	CAGARTCAAGTCCCAG GGG	201	PAG BA 190_ 209 R	CCTGTAGTAGAAGAGGTAA C	558
42	PAG BA 123 145 F	AGARTCAAGTCCCAGG GGTTAC	202	PAG BA 187_ 210 R	CCCTGTAGTAGAAGAGGTA ACCA	557
43	PAG BA 269 287 F	AATCTGCTATTGGTCA GG	203	PAG BA 326 344 R	TGATTATCAGCGGAAGTAG ACCA	559
44	PAG BA 655 675 F	GAAGATATACGGTTGA TCTC	204	PAG BA 755_ 772 R	CCGTGCTCCATTTTTCAG G	560
45	PAG BA 755 772 F	TCCTGA AAAATGGAGCA CGG	205	PAG BA 849_ 869 R	TCGGATAAGCTGCCACAAG G	561
46	PAG BA 763 781 F	TGGAGCAAGGCTTCTGA TC	206	PAG BA 849_ 869 R	TCGGATAAGCTGCCACAAG G	562
912	PARC X9581 9_123_147_ F	GGCTCAGCCATTAGTT ACCGCTAT	207	PARC X95819 232 260 R	TGCTCAGCAATAATTCAC TATAGCCGA	566
913	PARC X9581 9_143_63 F	TCAGCGGTACAGTGGG TGCT	208	PARC X95819 143 170 R	TTCCCTGACCTTCGATTA AAGGATAGC	563
911	PARC X9581 9_97 110 F	TGGTGAATCGGCATGTT ATGAAGC	209	PARC X95819 192 219 R	GGTATAAGCATCGCACA AAGATTTA	564
910	PARC X9581 9_97 110 F	TGGTGAATCGGCATGTT ATGAAGC	209	PARC X95819 201 222 R	TTGGTATAAGCATCGCA GCA	565
773	PLA AF0539 45_7186_72 11 F	TTATACCGGAACCTCC CGAAGGAG	210	PLA AF05394 5_7257_7280 R	TAATGCGATACTGGCTCG AAGTC	567
770	PLA AF0539 45_7377_74 02 F	TGACATCCGGCTCACGT TATATGGT	211	PLA AF05394 5_7434_7462 R	TGTAATTTCCGCAAGACT TTGGCATAG	568
771	PLA AF0539 45_7382_74 04 F	TCGGCTCAGCTTATTA TGGTAC	212	PLA AF05394 5_7482_7502 R	TGGTCTGAGTACCTCCTTT GC	569
772	PLA AF0539 45_7481_75 03 F	TGCAAGAGGATCTCA GACCAT	213	PLA AF05394 5_7539_7562 R	TATTTGGAATACCGGCAGC ATCTC	570
909	RECA AF251 469_169_21 0 F	TGACATGCTTTCCGCT CAGGC	214	RECA AF2514 69_277_300 R	TGGCTCATAAGAGCGCTT GTAGA	572
908	RECA AF251 469_43_68 F	TGGTACATGTGCTTCA TTGATGCTG	215	RECA AF2514 69_140_163 R	TTCAAGTGTGTGCTCACCA TTGTG	571
1072	RNASEP BDP 574 592 F	TGGCAGCGCATCTCG TG	216	RNASEP BDP 616 635 R	TGCTTTACCCCTGTCTATC CG	573
1070	RNASEP BRM 580 599 F	TGCGGTAGGGAGCTTG AGC	217	RNASEP BRM 665 686 R	TCGGATAAGCGGATCTTG TGC	574
1071	RNASEP BRM 616 637 F	TCTTAGGAAGATGGCTG CCAGC	218	RNASEP BRM 665 687 R	TGCGGATAAGCGGATTTCT GTGC	575
1112	RNASEP BRM 325 347 F	TACGCGAGGAAGTGCT CACAGA	219	RNASEP BRM 402 428 R	TCTCTTACCCACCCCTTTC ACCTTAC	576
1172	RNASEP BRM 461 488 F	TAAACCCCATCGGGAGC AAGACCGAATA	220	RNASEP BRM 542 561 2 R	TGCTCTGGTCAACCCACCC G	577
1111	RNASEP BRM 461 488 F	TAAACCCCATCGGGAGC AAGACCGAATA	220	RNASEP BRM 542 561 R	TGCTCTGGTCAACCCACCC G	578
258	RNASEP BS 43 61 F	GAGGAAGTCCATGCTC GC	221	RNASEP BS 3 63 384 R	GTAAGCATGTTTTTGTTC ATC	579
259	RNASEP BS 43 61 F	GAGGAAGTCCATGCTC GC	221	RNASEP BS 3 63 384 R	GTAAGCATGTTTTTGTTC ATC	579
258	RNASEP BS 43 61 F	GAGGAAGTCCATGCTC GC	221	RNASEP EC 3 45 362 R	ATAAGCCGGGTTCTGTG	581

258	RNASEP_BS_43 61 F	GAGGAAAGTCCATGCTCGC	221	RNASEP_SA_3 58 379 R	ATAAGCCATGTTCTGTTC	584
1076	RNASEP_CLB_459 487 F	TAAAGATATGCAACAGAGATATACCGC	222	RNASEP_CLB_498 522 R	TTTACCTGCGCTTCCACCCTTACC	579
1075	RNASEP_CLB_459 487 F	TAAAGATATGCAACAGAGATATACCGC	222	RNASEP_CLB_498 522 R	TGCTCTTACCTCACCGTTCACCTTAC	580
258	RNASEP_EC_61 77 F	GAGGAAAGTCCGGGCTC	223	RNASEP_BS_3 63 384 R	CTAAGCCATGTTTGTTC	578
258	RNASEP_EC_61 77 F	GAGGAAAGTCCGGGCTC	223	RNASEP_EC_3 45 362 R	ATAAGCCGGGTCTGTGC	581
260	RNASEP_EC_61 77 F	GAGGAAAGTCCGGGCTC	223	RNASEP_EC_3 45 362 R	ATAAGCCGGGTCTGTGC	581
258	RNASEP_EC_61 77 F	GAGGAAAGTCCGGGCTC	223	RNASEP_SA_3 58 379 R	ATAAGCCATGTTCTGTTC	584
1085	RNASEP_RKP_264 287 F	TCCTAATGGTCTGCAGTGGG	224	RNASEP_RKP_295 321 R	TCCTATAGTCCGGACTTCTCTGTA	582
1082	RNASEP_RKP_419 448 F	TGCTATAGCGCCACCGGTAACCTTGTGTACA	225	RNASEP_RKP_542 565 R	TCAGCGATCTACCCGCAT	583
1083	RNASEP_RKP_422 443 F	TAAAGCGCACCGGTAACTGG	226	RNASEP_RKP_542 565 R	TCAGCGATCTACCCGCAT	583
1086	RNASEP_RKP_426 446 F	TGCTATACCGGTAACTGGCAACA	227	RNASEP_RKP_542 565 R	TCAGCGATCTACCCGCAT	583
1084	RNASEP_RKP_466 491 F	TCACCCAAAGGCAAGATCAATAGG	228	RNASEP_RKP_542 565 R	TCAGCGATCTACCCGCAT	583
258	RNASEP_SA_31 49 F	GAGGAAAGTCCATGCTCAC	229	RNASEP_BS_3 63 384 R	GTAAGCCATGTTTGTTC	578
258	RNASEP_SA_31 49 F	GAGGAAAGTCCATGCTCAC	229	RNASEP_EC_3 45 362 R	ATAAGCCGGGTCTGTGC	581
258	RNASEP_SA_31 49 F	GAGGAAAGTCCATGCTCAC	229	RNASEP_SA_3 58 379 R	ATAAGCCATGTTCTGTTC	584
262	RNASEP_SA_31 49 F	GAGGAAAGTCCATGCTCAC	229	RNASEP_SA_3 58 379 R	ATAAGCCATGTTCTGTTC	584
1098	RNASEP_VBC_331 349 F	TCGCGGAGTTGACTGGGT	230	RNASEP_VBC_388 414 R	TGACTTTCTCCOCCCTTATCAGTCTCC	585
66	RPLB_EC_65 0 679 F	GACCTACAGTAAGAGTCTGTATGAACC	231	RPLB_EC_739 762 R	TCCTAGTGTGGTTTACCCCATGG	591
356	RPLB_EC_65 0 679 F	TGACCTACAGTAAGAGTCTGTATGAACC	232	RPLB_EC_739 762 R	TCCTAGTGTGGTTTACCCCATGG	592
73	RPLB_EC_66 9 698 F	TGTATAGAACCTTAATGACCATCCACCGG	233	RPLB_EC_735 761 R	CCAGTGTGGTTTACCCCATGG	586
74	RPLB_EC_67 1 700 F	TAAATGACCCCTTAATGACCATCCACCGG	234	RPLB_EC_737 762 R	TCCTAGTGTGGTTTACCCCATGG	590
67	RPLB_EC_68 8 710 F	CATCCACACGGTGGTGGTGAAGG	235	RPLB_EC_736 757 R	GTGCTGGTTTACCCCATGGAGT	587
70	RPLB_EC_68 8 710 F	CATCCACACGGTGGTGGTGAAGG	235	RPLB_EC_743 771 R	TGTTTTGTATCCCAAGTGTGTTTACCC	593
357	RPLB_EC_68 8 710 F	TCATCCACACGGTGGTGGTGAAGG	236	RPLB_EC_736 757 R	TGTGCTGGTTTACCCCATGGAGT	588
449	RPLB_EC_69 0 710 F	TCACACCGGTGGTGGTGAAGG	237	RPLB_EC_737 758 R	TGTGCTGGTTTACCCCATGGAGT	589
113	RPOB_EC_13 36 1353 F	GACCACTCCGCAACCGT	238	RPOB_EC_143 8 1455 R	TTGCTCTCGGCTGGGC	594
963	RPOB_EC_15 27 1549 F	TCAGCTGTGCGAGTTTCA	239	RPOB_EC_163 0 1649 R	TGCTGCGGAGTTTGAAGC	595
72	RPOB_EC_18 45 1866 F	TGCTGCTCAGCGCAACTCCAAC	240	RPOB_EC_190 9 1929 R	CGCTGATTGCGCTTGTCTACG	596
359	RPOB_EC_18 45 1866 F	TTATCGCTCAGCGCAACTCCAAC	241	RPOB_EC_190 9 1929 R	TGCTGGAITTCGCTTGTCTACG	597
962	RPOB_EC_20 05 2027 F	TCGTTCTGGAACACGATGACGC	242	RPOB_EC_204 1 2064 R	TTGACGTTGCACTGTTCGAGCCCAT	598
69	RPOB_EC_37 62 3790 F	TCACCAACCTCTTGGAGGTAAAGCTCACT	243	RPOB_EC_383 6 3865 R	TTTCTTGAAGAGTATGAGCTGCTCGTAAG	600
111	RPOB_EC_37 75 3803 F	CTTGGAGCTTACTGTCTATTTGGGAGCA	244	RPOB_EC_382 9 3858 R	CGATATAGCTGCACCATAACTTGTATAGC	599
940	RPOB_EC_37 98 3821 F	TGGCGACGGTTTCGGCGCAATATGA	245	RPOB_EC_386 2 3889 R	TGTCCGACTTGACGGTATGCAITTTCTG	604
939	RPOB_EC_37 98 3821 F	TGGCGACGGTTTCGGCGCAATATGA	245	RPOB_EC_386 2 3889 R	TGTCCGACTTGACGGTATGCAITTTCTG	605
289	RPOB_EC_37 99 3821 F	GGGACGCGTTTCGGCGCAATATGA	246	RPOB_EC_386 2 3888 R	GTCCGACTTGACGGTCAACATTTCTG	602
362	RPOB_EC_37 99 3821 F	TGGCGACGGTTTCGGCGCAATATGA	245	RPOB_EC_386 2 3888 R	TGTCCGACTTGACGGTCAACATTTCTG	603

	OD F		R			
288	RPOB_EC_38 02_3821 F	CAGCGTTTCGGCGAAT GGA	247	RPOB_EC_386 2_3885 R	CGACTTGACGGTTACATT TCCTG	601
48	RPOC_EC_10 18_1045_2 F	CAAACTTATTAGGTAA GGCGTTGACT	248	RPOC_EC_109 5_1124_2 R	TCAGCGGCATTCTCTTCG GTAAACCAAT	610
47	RPOC_EC_10 18_1045 F	CAAACTTATTAGGTAA GGCGTTGACT	248	RPOC_EC_109 5_1124 R	TCAGCGGCATTCTCTTCG GTAAACCAAT	611
68	RPOC_EC_10 36_1060 F	CGGTGTGACTATTCCGG GGGTTCAG	249	RPOC_EC_109 7_1126 R	ATTCAGAGCCATTCTCTT TGGTAACCAAC	612
49	RPOC_EC_11 4_140 F	TAAGAAGCCGGAACCA TCAACTACCG	250	RPOC_EC_213 232 R	GGCGCTTGACTTACCGCA C	617
227	RPOC_EC_12 56_1277 F	ACCGACTGCTGCTGAAC CGTGC	251	RPOC_EC_129 5_1315 R	GTTCAAATGCTGGATACC CA	613
292	RPOC_EC_13 74_1393 F	CGCGACTTCGACGGTG ACC	252	RPOC_EC_143 7_1455 R	GAGCATCAGCGTGCGTCT T	614
364	RPOC_EC_13 74_1393_TM OD F	TCGCGCACTTCGACGGT GACC	253	RPOC_EC_143 7_1455_TM OD R	TGAGCATCAGCGTGCGTCT T	615
229	RPOC_EC_15 84_1604 F	TGGCCGAAAGAGCTG ACGG	254	RPOC_EC_162 3_1643 R	ACGCGGGCATGACAGATG CC	616
978	RPOC_EC_21 45_2175 F	TCAGGATCGTTCAACT CGATCTACATGATG	255	RPOC_EC_222 8_2247 R	TTACGOCATCAGGCCACGC A	622
290	RPOC_EC_21 46_2174 F	CAGGAGTGGTCAACTC GATCTACATGAT	256	RPOC_EC_222 7_2245 R	ACGCCATCAGGCCACGCAT T	620
363	RPOC_EC_21 46_2174_TM OD F	TCAGGAGTGGTCAACT CGATCTACATGAT	257	RPOC_EC_222 7_2245_TM OD R	TACGCCATCAGGCCAAGCA T	621
51	RPOC_EC_21 78_2196_2 F	TGATTCCGGTGGCCCGTG GT	258	RPOC_EC_222 5_2246_2 R	TTGGCCATCAGACCACGCA TAC	618
50	RPOC_EC_21 78_2196 F	TGATTCTGGTGGCCCGTG GT	259	RPOC_EC_222 5_2246 R	TTGGCCATCAGGCCACGCA TAC	619
53	RPOC_EC_22 18_2241_2 F	CTTGCTGGTATGGGTGG TCTGATG	260	RPOC_EC_231 3_2337_2 R	CGCACCATGCGTAGAGATG AAGTAC	623
52	RPOC_EC_22 18_2241 F	CTTGCGAGGTATGGGTGG TCTGATG	261	RPOC_EC_231 3_2337 R	CGCACCATGCGGTGGTAGATG AAGTAC	624
354	RPOC_EC_22 18_2241_TM OD F	CTTGCGAGGTATGGGTGG TCTGATG	262	RPOC_EC_231 3_2337_TM OD R	TCGCACCGTGGGTGGTAGAT GAGTAC	625
958	RPOC_EC_22 23_2243 F	TGGTATGCGTGGTCTGTA TGGC	263	RPOC_EC_232 9_2352 R	TGCTAGACCTTTACGTGCA CCGTG	626
960	RPOC_EC_23 34_2357 F	TGCTCGTAAGGGTCTGG CGGATAC	264	RPOC_EC_238 0_2403 R	TAACTAGACGACGGGTACAG TAAAC	627
55	RPOC_EC_80 8_833_2 F	CGTGGGTGTAATTACCG TAACAACCG	265	RPOC_EC_865 891 R	AGCTTTTTCTGTTTGAACG ATAATGCT	629
54	RPOC_EC_80 8_833 F	CGTGGGTGTAATTACCG TAACAACCG	266	RPOC_EC_865 899 R	GTTTTTCTGCGTACATGAT GATGTC	628
961	RPOC_EC_91 7_938 F	TATTTGGACAACGGTCT CGCGG	267	RPOC_EC_100 9_1034 R	TTACCGACGAGGTTCTGAC GGAAACG	607
959	RPOC_EC_91 8_938 F	TCTGGATAACGGTCTCT GGGG	268	RPOC_EC_100 9_1031 R	TCGACGAGGTTCTGACGGA AAGC	606
57	RPOC_EC_99 3_1019_2 F	CAAGGTTAAGCAAGGAC GTTCGCTCA	269	RPOC_EC_103 6_1059_2 R	CGAACGGCCAGAGTAGTCA ACACG	608
56	RPOC_EC_99 3_1019 F	CAAGGTTAAGCAAGGAC GTTCGCTCA	270	RPOC_EC_103 6_1059 R	CGAACGGCCAGTAGTAGTCA ACACG	609
75	SP101_SPET 11_1_29 F	AACTCTAATTTGGAAGA AACCCAGAAGT	271	SP101_SPET1 1_92_116 R	CTCAACCAAGCTTACCAAA GGGAC	676
446	SP101_SPET 11_1_29_TM OD F	TAACTCTAATTTGGAAGA AACCCAGAAGT	272	SP101_SPET1 1_92_116_TM OD R	TCCTACCAACAGTTCACCA AGGSCAG	677
85	SP101_SPET 11_1154_11 79 F	CAATACCGCAACACGG TGCGTTGGG	273	SP101_SPET1 1_1251_1277 R	GACCCCAACCTGGCCTTTT GTCTGTGA	630
424	SP101_SPET 11_1154_11 79_TM OD F	TCAATACCGCAACACGG GTGGCTTGGG	274	SP101_SPET1 1_1251_1277 TM OD R	TGACCCCAACCTGGCCTTT TGTCTGTGA	631
76	SP101_SPET 11_118_147 F	GCTGGTGAATAAACCC AGATGCTGCTTC	275	SP101_SPET1 1_213_238 R	TGTGGCCGATTTCACCAAC TGCTCT	644
425	SP101_SPET 11_118_147 TM OD R	TGCTGGTGAATAAACCC AGATGCTGCTTC	276	SP101_SPET1 1_213_238 TM OD R	TTGTGGCCGATTTCACCAAC CTGCTCT	645
86	SP101_SPET 11_118_147 TM OD R	CGCAAAAAATCCAGCT	277	SP101_SPET1 1_213_238 TM OD R	AAACTATTTTTTAGCTAT	632

	11_1314_13 36 F	ATTAGC		1_1403_1431 R	ACTCGAACAC	
426	SP101_SPET 11_1314_13 36 TMOD F	TGCGAAAAATCCAGC TATTAGC	278	SP101_SPET1 1_1403_1431 TMOD R	TAAACTATTTTTTAGCTA TACTCGAACAC	633
87	SP101_SPET 11_1408_14 37 F	CGAGTATAGCTAAAAA ATAGTTTATGACA	279	SP101_SPET1 1_1486_1515 R	GGATAA'T'GTGCTGAACAA GGGATAGTGAG	634
427	SP101_SPET 11_1408_14 37 TMOD F	TCGAGTATAGCTAAAAA AATAGTTTATGACA	280	SP101_SPET1 1_1486_1515 TMOD R	TGGATAAT'GTGCTGAACAA AGGGATAGTGAG	635
88	SP101_SPET 11_1688_17 16 F	CCATATATTAATCGTTTA CAGAACTGGCT	281	SP101_SPET1 1_1783_1808 R	ATATGATTATCAATTGAAC GCGGCCG	636
428	SP101_SPET 11_1688_17 16 TMOD F	TCCATATATTAATCGTTT ACAGAACTGGCT	282	SP101_SPET1 1_1783_1808 TMOD R	TATATGATTATCAATTGAAC TGCGGCCG	637
89	SP101_SPET 11_1711_17 33 F	CTGGCTAAACCTTTGGC AACGGT	283	SP101_SPET1 1_1808_1835 R	GCGTGACGACCTCTTGAA TTGTAATCA	638
429	SP101_SPET 11_1711_17 33 TMOD F	TCTGGCTAAACCTTTGG CAACGGT	284	SP101_SPET1 1_1808_1835 TMOD R	TGCGTGACGACCTCTTGGA ATTGTAATCA	639
90	SP101_SPET 11_1807_18 35 F	ATGATTACAATCAAGA AGGCTGTCACGC	285	SP101_SPET1 1_1901_1927 R	TTGGACCTGTATCAAGCTG AATACTGG	640
430	SP101_SPET 11_1807_18 35 TMOD F	TATGATTACAATCAAG AAGGCTGTCACGC	286	SP101_SPET1 1_1901_1927 TMOD R	TTTGGACCTGTATCAAGCT GAATACTGG	641
91	SP101_SPET 11_1967_19 91 F	TAACGGTTATCATGGCC CAGATGGG	287	SP101_SPET1 1_2062_2083 R	ATTGCCGCAAAATCAATC ATC	642
431	SP101_SPET 11_1967_19 91 TMOD F	TTAACGGTTATCATGGC CCAGATGGG	288	SP101_SPET1 1_2062_2083 TMOD R	TATTGCCGCAAAATCAAT CATC	643
77	SP101_SPET 11_216_243 F	AGCAGGTGGTGAATCG GCCACATGATT	289	SP101_SPET1 1_308_333 R	TGCCACTTTGCAACCTCT GTTGCTG	654
432	SP101_SPET 11_216_243 TMOD F	TAGCAGGTGGTGAATC GGCCACATGATT	290	SP101_SPET1 1_308_333 T MOD R	TTGCCACTTTGCAACCTCC TGTTGCTG	655
92	SP101_SPET 11_2260_22 83 F	CAGAGACCGTTTTATCC TATCAGC	291	SP101_SPET1 1_2375_2397 R	TCTGGGTGACCTGGGTGTT TAGA	646
433	SP101_SPET 11_2260_22 83 TMOD F	TCAGAGACCGTTTTATC CTATCAGC	292	SP101_SPET1 1_2375_2397 TMOD R	TTCTGGGTGACCTGGGT TTAGA	647
93	SP101_SPET 11_2375_23 99 F	TCTAAAACACAGGTCA CCCAGAG	293	SP101_SPET1 1_2470_2497 R	AGCTGCTAGATGAGCTTCT GCCATGGCC	648
434	SP101_SPET 11_2375_23 99 TMOD F	TTCTAAAACACAGGTCA ACCCAGAG	294	SP101_SPET1 1_2470_2497 TMOD R	TAGCTGCTAGATGAGCTTC TGCCATGGCC	649
94	SP101_SPET 11_2468_24 87 F	ATGGCCATGGCAGAGC TCA	295	SP101_SPET1 1_2543_2570 R	CCATAAGGTCAACCTGCACC ATTCAAAGC	650
435	SP101_SPET 11_2468_24 87 TMOD F	TATGGCCATGGCAGAG CTCA	296	SP101_SPET1 1_2543_2570 TMOD R	TCCATAAGGTCAACCTGCAC CATTCAAAGC	651
78	SP101_SPET 11_266_295 F	CTTGTACTTGTGGCTCA CACGGCTGTTGG	297	SP101_SPET1 1_355_380 R	GCTGCTTGTAGGCTGAAT CCCTCTC	661
436	SP101_SPET 11_266_295 TMOD F	TCTTGTACTTGTGGCTC ACACGGCTGTTGG	298	SP101_SPET1 1_355_380 T MOD R	TGCTGCTTGTAGGCTGA TCCCTCTC	662
95	SP101_SPET 11_2961_29 84 F	ACCATGACAGAAAGCAT TTTGACA	299	SP101_SPET1 1_3023_3045 R	GGATTTACCAGCGATAGA CACC	652
437	SP101_SPET 11_2961_29 84 TMOD F	TACCATGACAGAAAGCA TTTTGACA	300	SP101_SPET1 1_3023_3045 TMOD R	TGGAATTTACCAGCGATAG ACACC	653
96	SP101_SPET 11_3075_31 03 F	GATGACTTTTATAGCTAA GGTCAGGACGC	301	SP101_SPET1 1_3168_3196 R	AATCGACGACCATCTTGA AAGATTTCTC	656
438	SP101_SPET	TGATGACTTTTATAGCTA	302	SP101_SPET1	TAATCGACGACCACTTTGG	657

	11_3075_31 03 TMOD F	ATGGTCAGGCAGC		1_3168_3196 TMOD R	AAAGATTTCCTC	
448	SP101_SPT1 11_3085_31 04 F	TAGCTAATGGTCAGGCA GCC	303	SP101_SPT1 1_3170_3194 R	TGCAGCACCATTCTGAAA GATTTC	658
79	SP101_SPT1 11_322_344 F	GTCAAA GTGGCAGTTT ACTGGC	304	SP101_SPT1 1_423_441 R	ATCCCCCTGCTCTGCTGCC	665
439	SP101_SPT1 11_322_344 TMOD F	TGTCAAAGTGGCAGCTT TACTGGC	305	SP101_SPT1 1_423_441_T MOD R	TATCCCCCTGCTCTGCTGC C	666
97	SP101_SPT1 11_3386_34 03 F	AGCGTA AAGGTGAACCT T	306	SP101_SPT1 1_3480_3506 R	CCAGCAGTACTGTCCCTT CATCTTG	659
440	SP101_SPT1 11_3386_34 03 TMOD F	TAGCGTAAAGGTGAACC TT	307	SP101_SPT1 1_3480_3506 TMOD R	TCCAGCAGTACTGTCCCTT TCATCTTG	660
98	SP101_SPT1 11_3511_35 35 F	GCTTCAAGGAATCAATGA TGGAGCAG	308	SP101_SPT1 1_3605_3629 R	GGGTCTACACCTGCACCTTG CATAC	663
441	SP101_SPT1 11_3511_35 35 TMOD F	TGCTTCAGGAATCAATG ATGGAGCAG	309	SP101_SPT1 1_3605_3629 TMOD R	TGGGTCTACACCTGCACCTT GCATAC	664
80	SP101_SPT1 11_358_387 F	GGGGATTCAGGCATCAA AGCAGCTATTGAC	310	SP101_SPT1 1_448_473 R	CCACCTTTTCCACACAG AATCAGC	668
442	SP101_SPT1 11_358_387 TMOD F	TGGGGATTAGGCATCAA AAGCAGCTATTGAC	311	SP101_SPT1 1_448_473_T MOD R	TCCACCTTTTCCACACAG GAATCAGC	669
447	SP101_SPT1 11_364_385 F	TCAGCCATCAAGCAGC TATTG	312	SP101_SPT1 1_448_471 R	TACCTTTTCCACACAGAA TCAGC	667
81	SP101_SPT1 11_600_629 F	CCTTACTTCGAACTATG AATCTTTTGGAG	313	SP101_SPT1 1_686_714 R	CCATTTTTTCAAGCATGC TGAAATATC	670
443	SP101_SPT1 11_600_629 TMOD F	TCCTTACTTCGAACTAT GAATCTTTTGGAG	314	SP101_SPT1 1_686_714_T MOD R	TCCATTTTTCAGCATGC CTGAATATC	671
82	SP101_SPT1 11_658_684 F	GGGGATTCGATATCACCG ATAAGAAGAA	315	SP101_SPT1 1_756_784 R	GATTGGCGATAAAGTGATA TTTTCTAAA	672
444	SP101_SPT1 11_658_684 TMOD F	TGGGGATTGATATCACCC GATAAGAAGAA	316	SP101_SPT1 1_756_784_T MOD R	TGATTGGCGATAAAGTGAT AATTTCTAAA	673
83	SP101_SPT1 11_776_801 F	TCGCCAATCAAACTAA GGGAATGGC	317	SP101_SPT1 1_871_896 R	GCCACACAGAAAGACTAGC AGGATTA	674
445	SP101_SPT1 11_776_801 TMOD F	TTGCGCAATCAAACTAA AGGGAAATGGC	318	SP101_SPT1 1_871_896_T MOD R	TGCCACACAGAAAGACTAG CAGGATTA	675
84	SP101_SPT1 11_893_921 F	GGGCAACAGCAGCGGAT TGGGATTTGCGCG	319	SP101_SPT1 1_988_1012 R	CATGACAGCAAGACCTCA CCACCC	678
423	SP101_SPT1 11_893_921 TMOD F	TGGGCAACAGCAGCGGAA TTGCGAATTTGCGCG	320	SP101_SPT1 1_988_1012 TMOD R	TCATGACAGCAAGACCTCA ACCCACC	679
706	SSPE_BA_11 4_137 F	TCAGCAAAAGCCACAAT CAGAAGC	321	SSPE_BA_196 222 R	TTCACGCTCTGTTTCAGTT GCAATTC	683
612	SSPE_BA_11 4_137 F	TCAGCAAAAGCCACAAT CAGAAGC	321	SSPE_BA_196 222F R	TTGACGCTCTGTTTCAGTT GCAATTC	684
58	SSPE_BA_11 5_137 TMOD F	CAGCAAAAGCCACAAT CAGAAGC	322	SSPE_BA_197 222 R	TTCACGCTCTGTTTCAGTT CAATTC	686
355	SSPE_BA_11 5_137 TMOD F	TCAGCAAAAGCCACAAT CAGAAGC	321	SSPE_BA_197 222 TMOD R	TTGACGCTCTGTTTCAGTT GCAATTC	687
215	SSPE_BA_12 1_137 F	AAGCAACAATCAGAAGC	323	SSPE_BA_197 216 R	TCGTGTTTCAGTTGCAATTC C	685
699	SSPE_BA_12 3_153 F	TGCACAATCAGAAGCTA AGAAAGCCGACGCT	324	SSPE_BA_202 231 R	TTTTCACAGCATGACGCTCT GTTTCAGTTGC	688
704	SSPE_BA_14 6_168 F	TGCAGCTCTCTGTTGCT AGCATTT	325	SSPE_BA_242 267 R	TTTGATTTGTTTTCAGCT GATTTG	689
702	SSPE_BA_15 0_168 F	TGCTCTTGCTGCTAGCA TT	326	SSPE_BA_243 264 R	TGATTTTTCAGCTGAT TGT	691
610	SSPE_BA_15 0_168 F	TGCTCTTGCTGCTAGCA TT	326	SSPE_BA_243 264F R	TGATTTTTCAGTGTGAT CTCTGT	691

700	SSPE BA 15 6 168 F	TGGTGCCTAGCATTT	327	SSPE BA 243 255 R	TGCAGCTGATTGT	690
608	SSPE BA 15 6 168P F	TGGC*GU*CA*GU*ATT	327	SSPE BA 243 255P R	TGU*AGU*TGAC*C*GT	690
705	SSPE BA 63 89 F	TGCTAGTATAGGTACAG AGTTCGCAC	328	SSPE BA 163 191 R	TCATATACCTAGCATTTGTGC TTTGAAAGCT	682
703	SSPE BA 72 89 F	TGGTACAGATTTGCGA C	329	SSPE BA 163 182 R	TCATTTGTGCTTTGAATGC T	681
611	SSPE BA 72 89P F	TGGTAU*AGAGC*C*C*G U*GAC	329	SSPE BA 163 182P R	TCATTTGTGCC*C*C*GAAC *GU*T	681
701	SSPE BA 75 89 F	TACAGAG*TTTSCGAC	330	SSPE BA 163 177 R	TGTGCTTTTGAAATGCT	680
609	SSPE BA 75 89P F	TAU*AGAGC*C*C*CGU*G AC	330	SSPE BA 163 177P R	TGTGCC*C*C*GAAC*GU*T	680
1099	TOXR_VBC_1 35 156 F	TGGATTAGGCGACCAAG ARAGCCG	331	TOXR_VBC_22 1 246 R	TTCAAACCTTGGCTCTCGC CRAACAA	692
905	TRFE AY094 355 1064_1 086 F	TGCACTTTGGCAGGAA CTAGAC	332	TRFE AY0943 55 1171_119 6 R	TACATCGTTTGGCCCAAGA TCAATCA	693
904	TRFE AY094 355 1278_1 303 F	TCAAAATGTACAAGGTGA AGTGCCTGA	333	TRFE AY0943 55 1392_141 8 R	TCCTCTTTTACAGGCTCT ACTTCAFC	694
903	TRFE AY094 355 1445_1 471 F	TGGATGGCATGGTGAA TGGATATGTC	334	TRFE AY0943 55 1551_158 0 R	TATTTGGGTTTCAATCCAC TCAGATTCTGG	695
902	TRFE AY094 355 1467_1 491 F	ATGTGCATTCGAATCCG TACTTGTG	335	TRFE AY0943 55 1569_159 2 R	TGGCGAGCTTTTATTGGS GTTTC	696
906	TRFE AY094 355 666 68 8 F	GTGCATGCGGATACAGA CAGAG	336	TRFE AY0943 55 769_791 R	TTCAAATGCGGAGGCGTA TGTG	697
907	TRFE AY094 355 757_77 6 F	TGCAAGCGCGACCAT ACG	337	TRFE AY0943 55 864_883 R	TGCCAGGTACAACTGCA T	698
114	TUFB EC 22 5 251 F	GCACTATGCAACAGTAG ATTGTCTGG	338	TUFB EC 284 309 R	TATAGCAACCATCCATCGA CGCGAC	706
60	TUFB EC 23 9 259 2 F	TTGACTGCCAGGCTCAC GCTG	339	TUFB EC 283 303 2 R	CGCGTCCATTTGAGACGCA CC	704
59	TUFB EC 23 9 259 F	TAGACTGCCAGGACAC GCTG	340	TUFB EC 283 303 R	CGCGTCCATTTGAGACGCA CC	705
942	TUFB EC 25 1 278 F	TGCAAGCGCATATGTT ARGAATCATGAT	341	TUFB EC 337 360 R	TATGTGCTCACGATTTGCG GGCAT	707
941	TUFB EC 27 5 299 F	TGATCACTGGTGCTGCT CGATGGA	342	TUFB EC 337 362 R	TGGATGTGCTCACGAGTCT GTGGCAT	708
117	TUFB EC 75 7 774 F	ARGACGACCTGCACGGG C	343	TUFB EC 849 867 R	GGCGTCCAGCTTTTCAAGC G	709
293	TUFB EC 95 7 979 F	CCACAGCGCGTTCTTCA ACAACT	344	TUFB EC 103 4 1058 R	GGCATCAACATTTTCTTGT CCTTCG	700
367	TUFB EC 95 7 979 TMOD F	TCCACAGCGCGTTCTTC ARCAACT	345	TUFB EC 103 4 1058 TMOD R	TGGCATCAACATTTTCTTGT TCTTTCG	701
62	TUFB EC 97 6 1000 2 F	ARCTACCGTCTCTGAT CTACTTCC	346	TUFB EC 104 5 1068 2 R	GTGTGACACGAGCATTAAC ATTTC	702
61	TUFB EC 97 6 1000 F	ARCTACCGTCTCGCATGT CTACTTCC	347	TUFB EC 104 5 1068 R	GTGTGCGCAGGACATAAC ATTTC	703
63	TUFB EC 98 5 1012 F	CCACAGCTTCTACTTCCG TACTACTGAGC	348	TUFB EC 103 3 1062 R	TCCAGGATTAACCATTTCT ACTCTTCTCGG	699
225	VALS EC 11 05 1124 F	CGTGGGCGCGTGGTAT CGA	349	VALS EC 119 5 1214 R	ACGAACTGGATGTGCGCGT T	710
71	VALS EC 11 05 1124 F	CGTGGGCGCGTGGTAT CGA	349	VALS EC 119 5 1218 R	CGGTACGACATGGATGTGCG CGGTT	711
358	VALS EC 11 05 1124 TMO CD F	TGCTGGCGCGTGGTTA CG F	350	VALS EC 119 5 1218 TMOD R	TCCGTACGAACATGGATGTGCG CGCGTT	712
965	VALS EC 11 28 1151 F	TATGCTGACCGACGAGT GTGACTGT	351	VALS EC 123 1 1257 R	TGCGGCGATCCAGGAGAGT TACATGTT	713
112	VALS EC 18 33 1850 F	CCACGCGCTGCGCTTCA C	352	VALS EC 192 0 1943 R	CGGTCCACAGCTTGTGTCG AGAAG	714
116	VALS EC 19 20 1943 F	CTTCTGCAACAGCTGTG GGACCC	353	VALS EC 194 8 1970 R	TGCGATTCATCAGCACGA ASCG	715
295	VALS EC 61 0 649 F	ACCGACGACGAGGACCA GCT	354	VALS EC 705 727 R	TATAAACGACATCGTCAGG GTGA	716
931	WAAA 29692 5 2 29	TTCTTGCTTTTTCGTGAG TTCTGPRATG	355	WAAA 296925 115 138 R	CARGCGGTTTGCCTCAAT AGTCA	717
932	WAAA 29692	TGCACTGGTTTATGTC	356	WAAA 296925	TGGCAGGAGCTGACCTGT	718

	5_286_311_	TGTTTCAGT		_394_412_R	
	F				

[0095] Primer pair name codes and reference sequences are shown in Table 2. The primer name code typically represents the gene to which the given primer pair is targeted. The primer pair name includes coordinates with respect to a reference sequence defined by an extraction of a section of sequence or defined by a GenBank gi number, or the corresponding complementary sequence of the extraction, or the entire GenBank gi number as indicated by the label “no extraction.” Where “no extraction” is indicated for a reference sequence, the coordinates of a primer pair named to the reference sequence are with respect to the GenBank gi listing. Gene abbreviations are shown in bold type in the “Gene Name” column.

Table 2: Primer Name Codes and Reference Sequences

Primer name code	Gene Name	Organism	Reference GenBank gi number	Extracted gene coordinates of gi number	Extraction or entire gene SEQ ID NO:
16S_EC	16S rRNA (16S ribosomal gene)	<i>Escherichia coli</i>	16127994	4033120..4034661	719
23S_EC	23S rRNA (23S ribosomal gene)	<i>Escherichia coli</i>	16127994	4166220..4169123	720
CAPC_BA	capC (capsule biosynthesis gene)	<i>Bacillus anthracis</i>	6470151	Complement (55628..56074)	721
CYA_BA	cya (cyclic AMP gene)	<i>Bacillus anthracis</i>	4894216	Complement (154288..156626)	722
DNAK_EC	dnaK (chaperone dnaK gene)	<i>Escherichia coli</i>	16127994	12163..14079	723
GROL_EC	groL (chaperonin groL)	<i>Escherichia coli</i>	16127994	4368603..4370249	724
HFLB_EC	hflb (cell division protein peptidase ftsH)	<i>Escherichia coli</i>	16127994	Complement (3322645..3324576)	725
INFB_EC	infB (protein chain initiation factor infB gene)	<i>Escherichia coli</i>	16127994	Complement (3310983..3313655)	726
LEF_BA	lef (lethal factor)	<i>Bacillus anthracis</i>	21392688	Complement (149357..151786)	727
PAG_BA	pag (protective antigen)	<i>Bacillus anthracis</i>	21392688	143779..146073	728
RPLB_EC	rplB (50S ribosomal protein L2)	<i>Escherichia coli</i>	16127994	3449001..3448180	729
RPOB_EC	rpoB (DNA-directed RNA polymerase beta chain)	<i>Escherichia coli</i>	6127994	Complement 4178823..4182851	730
RPOC_EC	rpoC (DNA-directed RNA polymerase beta' chain)	<i>Escherichia coli</i>	16127994	4182928..4187151	731
SP101ET_SFET_1	Concatenation comprising: gki (glucose kinase) gtr (glutamine transporter protein) murI (glutamate racemase) mutS (DNA mismatch	Artificial Sequence* - partial gene sequences of <i>Streptococcus pyogenes</i>	15674250	Complement (1258294..1258791) complement (1236751..1237200) 312732..313169 Complement	732

	repair protein)			(1787602..1788007)	
	xpt (xanthine phosphoribosyl transferase)			930977..931425	
	yqil (acetyl-CoA-acetyl transferase)			129471..129903	
	tkt (transketolase)			1391844..1391386	
SSPE BA	sspE (small acid-soluble spore protein)	Bacillus anthracis	30253828	22 6496..226783	733
TUFB EC	tufB (Elongation factor Tu)	Escherichia coli	16127994	4173523..4174707	734
VALS EC	vals (Valyl-tRNA synthetase)	Escherichia coli	16127994	complement (4481405..4478550)	735
ASPS EC	asps (Aspartyl-tRNA synthetase)	Escherichia coli	16127994	complement (1946777..1948546)	736
CAF1 AF 053947	caf1 (capsular protein caf1)	Yersinia pestis	2996286	No extraction - GenBank coordinates used	-
INV U22 457	inv (invasin)	Yersinia pestis	1256565	74..3772	737
LL NC00 3143	Y. pestis specific chromosomal genes - difference region	Yersinia pestis	16120353	No extraction - GenBank coordinates used	-
BONTA_X 52066	BoNT/A (neurotoxin type A)	Clostridium botulinum	40381	77..3967	738
MECA_Y1 4051	mecA methicillin resistance gene	Staphylococcus aureus	2791983	No extraction - GenBank coordinates used	739
TRPE_AY 094355	trpE (anthranilate synthase (large component))	Acinetobacter baumannii	20853695	No extraction - GenBank coordinates used	740
RECA_AF 251469	recA (recombinase A)	Acinetobacter baumannii	9965210	No extraction - GenBank coordinates used	741
GYRA_AF 100557	gyrA (DNA gyrase subunit A)	Acinetobacter baumannii	4240540	No extraction - GenBank coordinates used	742
GYRB_AB 008700	gyrB (DNA gyrase subunit B)	Acinetobacter baumannii	4514436	No extraction - GenBank coordinates used	743
WAAA_Z9 6925	waaa (3-deoxy-D-manno-octulosonic acid transferase) Concatenation comprising:	Acinetobacter baumannii	2765828	No extraction - GenBank coordinates used	744
CJST_CJ	tkt (transketolase)	Artificial Sequence* - partial gene sequences of Campylobacter jejuni		15 69415..1569873	
	glyA (serine hydroxymethyltransferase)		15791399	367573..368079	
	gltA (citrate synthase)			complement (1604529..1604930)	
	aspA (aspartate ammonia lyase)			96 692..97168	745
	glnA (glutamine synthase)			complement (657609..658085)	
	pgm (phosphoglycerate mutase)			32 7773..328270	

	uncA (ATP synthetase alpha chain)				112163..112651	
RNASEP_DDP	RNase (ribonuclease P)	P	Bordetella pertussis	33591275	Complement (3226720..3227933)	746
RNASEP_RKM	RNase (ribonuclease P)	P	Burkholderia mallei	53723370	Complement (2527296..2528220)	747
RNASEP_BS	RNase (ribonuclease P)	P	Bacillus subtilis	16077068	Complement (2330250..2330962)	748
RNASEP_CLB	RNase (ribonuclease P)	P	Clostridium perfringens	18308982	Complement (2291757..2292584)	749
RNASEP_EC	RNase (ribonuclease P)	P	Escherichia coli	16127994	Complement (3267457..3268233)	750
RNASEP_RKP	RNase (ribonuclease P)	P	Rickettsia prowazekii	15603881	complement(605276..606109)	751
RNASEP_SA	RNase (ribonuclease P)	P	Staphylococcus aureus	15922990	complement(1559869..1560651)	752
RNASEP_VBC	RNase (ribonuclease P)	P	Vibrio cholerae	15640032	complement(2580367..2581452)	753
ICD_CXB	icd (isocitrate dehydrogenase)		Coxiella burnetii	29732244	complement(1143867..1144235)	754
IS1111A	multi-locus IS1111A insertion element		Acinetobacter baumannii	29732244		-
OMPA_AY485227	ompA (outer membrane protein A)		Rickettsia prowazekii	40287451	No extraction	755
OMPB_RKF	ompB (outer membrane protein B)		Rickettsia prowazekii	15603881	complement(881264..886195)	756
GLTA_RKF	glta (citrate synthase)		Vibrio cholerae	15603881	complement(1062547..1063857)	757
TOXR_VBC	toxR (transcription regulator toxR)		Francisella tularensis	15640032	complement(1047143..1048024)	758
ASD_FRT	asd (Aspartate semialdehyde dehydrogenase)		Francisella tularensis	56707187	complement(438608..439702)	759
GALF_FR_T	galE (UDP-glucose 4-epimerase)		Shigella flexneri	56707187	809039..810058	760
IPAH_SGF	ipah (invasion plasmid antigen)		Campylobacter jejuni	30061571	2210775..2211614	761
HUPB_CJ	hupB (DNA-binding protein Hx-beta)		Coxiella burnetii	15791399	complement(849317..849819)	762
	Concatenation comprising:		Artificial Sequence* - partial gene sequences of Acinetobacter baumannii			763
AB_MLST	trpB (anthranilate synthase component I) adk (adenylate kinase) mutY (adenine glycosylase) fumC (fumarate hydratase) efp (elongation factor p) ppa (pyrophosphate phospho-hydratase)		-		Sequenced in-house	

[0096] * Note: These artificial reference sequences represent concatenations of partial gene extractions from the indicated reference gi number. Partial sequences were used to create the concatenated sequence because complete gene sequences were not necessary for primer design. The stretches of arbitrary residues "N"s were added for the convenience of separation of the partial gene extractions (100N for SP101_SPET11 (SEQ ID NO: 732); 50N for CJST_CJ (SEQ ID NO: 745); and 40N for AB_MLST (SEQ ID NO: 763)).

[0097] Example 2: DNA isolation and Amplification

[0098] Genomic materials from culture samples or swabs were prepared using the DNeasy® 96 Tissue Kit (Qiagen, Valencia, CA). All PCR reactions are assembled in 50 µl reactions in the 96 well microtiter plate format using a Packard MPII liquid handling robotic platform and MJ Dyad® thermocyclers (MJ research, Waltham, MA). The PCR reaction consisted of 4 units of Amplitaq Gold®, 1x buffer II (Applied Biosystems, Foster City, CA), 1.5 mM MgCl₂, 0.4 M betaine, 800 µM dNTP mix, and 250 nM of each primer.

[0099] The following PCR conditions were used to amplify the sequences used for mass spectrometry analysis: 95C for 10 minutes followed by 8 cycles of 95C for 30 seconds, 48C for 30 seconds, and 72C for 30 seconds, with the 48C annealing temperature increased 0.9C after each cycle. The PCR was then continued for 37 additional cycles of 95C for 15 seconds, 56C for 20 seconds, and 72C for 20 seconds.

[0100] Example 3: Solution Capture Purification of PCR Products for Mass Spectrometry with Ion Exchange Resin-Magnetic Beads

[0101] For solution capture of nucleic acids with ion exchange resin linked to magnetic beads, 25 µl of a 2.5 mg/mL suspension of BioClon amine terminated supraparamagnetic beads were added to 25 to 50 µl of a PCR reaction containing approximately 10 pM of a typical PCR amplification product. The above suspension was mixed for approximately 5 minutes by vortexing or pipetting, after which the liquid was removed after using a magnetic separator. The beads containing bound PCR amplification product were then washed 3x with 50mM ammonium bicarbonate/50% MeOH or 100mM ammonium bicarbonate/50% MeOH, followed by three more washes with 50% MeOH. The bound PCR amplicon was eluted with 25mM piperidine, 25mM imidazole, 35% MeOH, plus peptide calibration standards.

[0102] Example 4: Mass Spectrometry and Base Composition Analysis

[0103] The ESI-FTICR mass spectrometer is based on a Bruker Daltonics (Billerica, MA) Apex II 70e electrospray ionization Fourier transform ion cyclotron resonance mass spectrometer that employs an actively shielded 7 Tesla superconducting magnet. The active shielding constrains the majority of the fringing magnetic field from the superconducting magnet to a relatively small volume. Thus, components that might be adversely affected by stray magnetic fields, such as CRT monitors, robotic components, and other electronics, can operate in close proximity to the FTICR spectrometer. All aspects of pulse sequence control and data acquisition were performed on a 600 MHz Pentium II data station running Bruker's Xmass software under Windows NT 4.0 operating system. Sample aliquots, typically 1.5 μ l, were extracted directly from 96-well microtiter plates using a CTC HTS PAL autosampler (LEAP Technologies, Carrboro, NC) triggered by the FTICR data station. Samples were injected directly into a 10 μ l sample loop integrated with a fluidics handling system that supplies the 100 μ l/hr flow rate to the ESI source. Ions were formed via electrospray ionization in a modified Analytica (Branford, CT) source employing an off axis, grounded electrospray probe positioned approximately 1.5 cm from the metalized terminus of a glass desolvation capillary. The atmospheric pressure end of the glass capillary was biased at 6000 V relative to the ESI needle during data acquisition. A counter-current flow of dry N₂ was employed to assist in the desolvation process. Ions were accumulated in an external ion reservoir comprised of an rf-only hexapole, a skimmer cone, and an auxiliary gate electrode, prior to injection into the trapped ion cell where they were mass analyzed. Ionization duty cycles > 99% were achieved by simultaneously accumulating ions in the external ion reservoir during ion detection. Each detection event consisted of 1M data points digitized over 2.3 s. To improve the signal-to-noise ratio (S/N), 32 scans were co-added for a total data acquisition time of 74 s.

[0104] The ESI-TOF mass spectrometer is based on a Bruker Daltonics MicroTOF™. Ions from the ESI source undergo orthogonal ion extraction and are focused in a reflectron prior to detection. The TOF and FTICR are equipped with the same automated sample handling and fluidics described above. Ions are formed in the standard MicroTOF™ ESI source that is equipped with the same off-axis sprayer and glass capillary as the FTICR ESI source. Consequently, source conditions were the same as those described above. External ion accumulation was also employed to improve ionization duty cycle during data acquisition. Each detection event on the TOF was comprised of 75,000 data points digitized over 75 μ s.

[0105] The sample delivery scheme allows sample aliquots to be rapidly injected into the electrospray source at high flow rate and subsequently be electrosprayed at a much lower flow rate for improved ESI sensitivity. Prior to injecting a sample, a bolus of buffer was injected at a high flow rate to rinse the transfer line and spray needle to avoid sample contamination/carryover. Following the rinse step, the autosampler injected the next sample and the flow rate was switched to low flow. Following a brief equilibration delay, data acquisition commenced. As spectra were co-added, the autosampler continued rinsing the syringe and picking up buffer to rinse the injector and sample transfer line. In general, two syringe rinses and one injector rinse were required to minimize sample carryover. During a routine screening protocol a new sample mixture was injected every 106 seconds. More recently a fast wash station for the syringe needle has been implemented which, when combined with shorter acquisition times, facilitates the acquisition of mass spectra at a rate of just under one spectrum/minute.

[0106] Raw mass spectra were post-calibrated with an internal mass standard and deconvoluted to monoisotopic molecular masses. Unambiguous base compositions were derived from the exact mass measurements of the complementary single-stranded oligonucleotides. Quantitative results are obtained by comparing the peak heights with an internal PCR calibration standard present in every PCR well at 500 molecules per well for the ribosomal DNA-targeted primers and 100 molecules per well for the protein-encoding gene targets. Calibration methods are commonly owned and disclosed in U.S. Provisional Patent Application Serial No. 60/545,425.

[0107] Example 5: *De Novo* Determination of Base Composition of Amplification Products using Molecular Mass Modified Deoxynucleotide Triphosphates

[0108] Because the molecular masses of the four natural nucleobases have a relatively narrow molecular mass range (A = 313.058, G = 329.052, C = 289.046, T = 304.046 – See Table 3), a persistent source of ambiguity in assignment of base composition can occur as follows: two nucleic acid strands having different base composition may have a difference of about 1 Da when the base composition difference between the two strands is $G \leftrightarrow A$ (-15.994) combined with $C \leftrightarrow T$ (+15.000). For example, one 99-mer nucleic acid strand having a base composition of $A_{27}G_{30}C_{21}T_{21}$ has a theoretical molecular mass of 30779.058 while another 99-mer nucleic acid strand having a base composition of $A_{26}G_{31}C_{22}T_{20}$ has a theoretical molecular mass of 30780.052. A 1 Da difference in molecular mass may be within the experimental error of a

molecular mass measurement and thus, the relatively narrow molecular mass range of the four natural nucleobases imposes an uncertainty factor.

[0109] The present invention provides for a means for removing this theoretical 1 Da uncertainty factor through amplification of a nucleic acid with one mass-tagged nucleobase and three natural nucleobases. The term "nucleobase" as used herein is synonymous with other terms in use in the art including "nucleotide," "deoxynucleotide," "nucleotide residue," "deoxynucleotide residue," "nucleotide triphosphate (NTP)," or deoxynucleotide triphosphate (dNTP).

[0110] Addition of significant mass to one of the 4 nucleobases (dNTPs) in an amplification reaction, or in the primers themselves, will result in a significant difference in mass of the resulting amplification product (significantly greater than 1 Da) arising from ambiguities arising from the $G \leftrightarrow A$ combined with $C \leftrightarrow T$ event (Table 3). Thus, the same the $G \leftrightarrow A$ (-15.994) event combined with 5-Iodo-C $\leftrightarrow T$ (-110.900) event would result in a molecular mass difference of 126.894. If the molecular mass of the base composition $A_{27}G_{30}5\text{-Iodo-C}_{21}T_{21}$ (33422.958) is compared with $A_{26}G_{31}5\text{-Iodo-C}_{22}T_{20}$, (33549.852) the theoretical molecular mass difference is +126.894. The experimental error of a molecular mass measurement is not significant with regard to this molecular mass difference. Furthermore, the only base composition consistent with a measured molecular mass of the 99-mer nucleic acid is $A_{27}G_{30}5\text{-Iodo-C}_{21}T_{21}$. In contrast, the analogous amplification without the mass tag has 18 possible base compositions.

Table 3: Molecular Masses of Natural Nucleobases and the Mass-Modified Nucleobase 5-Iodo-C and Molecular Mass Differences Resulting from Transitions

Nucleobase	Molecular Mass	Transition	Δ Molecular Mass
A	313.058	A \rightarrow T	-9.012
A	313.058	A \rightarrow C	-24.012
A	313.058	A \rightarrow 5-Iodo-C	101.888
A	313.058	A \rightarrow G	15.994
T	304.046	T \rightarrow A	9.012
T	304.046	T \rightarrow C	-15.000
T	304.046	T \rightarrow 5-Iodo-C	110.900
T	304.046	T \rightarrow G	25.006
C	289.046	C \rightarrow A	24.012
C	289.046	C \rightarrow T	15.000
C	289.046	C \rightarrow G	40.006

5-Iodo-C	414.946	5-Iodo-C-->A	-101.888
5-Iodo-C	414.946	5-Iodo-C-->T	-110.900
5-Iodo-C	414.946	5-Iodo-C-->G	-85.894
G	329.052	G-->A	-15.994
G	329.052	G-->T	-25.006
G	329.052	G-->C	-40.006
G	329.052	G-->5-Iodo-C	85.894

[0111] Example 6: Data Processing

[0112] Mass spectra of bioagent identifying amplicons are analyzed independently using a maximum-likelihood processor, such as is widely used in radar signal processing. This processor, referred to as GenX, first makes maximum likelihood estimates of the input to the mass spectrometer for each primer by running matched filters for each base composition aggregate on the input data. This includes the GenX response to a calibrant for each primer.

[0113] The algorithm emphasizes performance predictions culminating in probability-of-detection versus probability-of-false-alarm plots for conditions involving complex backgrounds of naturally occurring organisms and environmental contaminants. Matched filters consist of *a priori* expectations of signal values given the set of primers used for each of the bioagents. A genomic sequence database is used to define the mass base count matched filters. The database contains the sequences of known bacterial bioagents and includes threat organisms as well as benign background organisms. The latter is used to estimate and subtract the spectral signature produced by the background organisms. A maximum likelihood detection of known background organisms is implemented using matched filters and a running-sum estimate of the noise covariance. Background signal strengths are estimated and used along with the matched filters to form signatures which are then subtracted. The maximum likelihood process is applied to this "cleaned up" data in a similar manner employing matched filters for the organisms and a running-sum estimate of the noise-covariance for the cleaned up data.

[0114] The amplitudes of all base compositions of bioagent identifying amplicons for each primer are calibrated and a final maximum likelihood amplitude estimate per organism is made based upon the multiple single primer estimates. Models of all system noise are factored into this two-stage maximum likelihood calculation. The processor reports the number of molecules of each base composition contained in the spectra. The quantity of amplification product

corresponding to the appropriate primer set is reported as well as the quantities of primers remaining upon completion of the amplification reaction.

[0115] Example 7: Use of Broad Range Survey and Division Wide Primer Pairs for Identification of Bacteria in an Epidemic Surveillance Investigation

[0116] This investigation employed a set of 16 primer pairs which is herein designated the "surveillance primer set" and comprises broad range survey primer pairs, division wide primer pairs and a single *Bacillus* clade primer pair. The surveillance primer set is shown in Table 4 and consists of primer pairs originally listed in Table 1. This surveillance set comprises primers with T modifications (note TMOD designation in primer names) which constitutes a functional improvement with regard to prevention of non-templated adenylation (*vide supra*) relative to originally selected primers which are displayed below in the same row. Primer pair 449 (non-T modified) has been modified twice. Its predecessors are primer pairs 70 and 357, displayed below in the same row. Primer pair 360 has also been modified twice and its predecessors are primer pairs 17 and 118.

Table 4: Bacterial Primer Pairs of the Surveillance Primer Set

Primer Pair No.	Forward Primer Name	Forward Primer (SEQ ID NO:)	Reverse Primer Name	Reverse Primer (SEQ ID NO:)	Target Gene
346	16S_EC_713_732_TMOD_F	27	16S_EC_789_809_TMOD_R	389	16S rRNA
10	16S_EC_713_732_F	26	16S_EC_789_809	388	16S rRNA
347	16S_EC_785_806_TMOD_F	30	16S_EC_880_897_TMOD_R	392	16S rRNA
11	16S_EC_785_806_F	29	16S_EC_880_897_R	391	16S rRNA
348	16S_EC_960_981_TMOD_F	38	16S_EC_1054_1073_TMOD_R	363	16S rRNA
14	16S_EC_960_981_F	37	16S_EC_1054_1073_R	362	16S rRNA
349	23S_EC_1826_1843_TMOD_F	49	23S_EC_1906_1924_TMOD_R	405	23S rRNA
16	23S_EC_1826_1843_F	48	23S_EC_1906_1924_R	404	23S rRNA
352	INFB_EC_1365_1393_TMOD_F	161	INFB_EC_1439_1467_TMOD_R	516	infb
34	INFB_EC_1365_1393_F	160	INFB_EC_1439_1467_R	515	infb
354	RPOC_EC_2218_2241_TMOD_F	262	RPOC_EC_2313_2337_TMOD_R	625	rpoC
52	RPOC_EC_2218_2241_F	261	RPOC_EC_2313_2337_R	624	rpoC
355	SSPE_BA_115_137_TMOD_F	321	SSPE_BA_197_222_TMOD_R	687	sspE
58	SSPE_BA_115_137_F	322	SSPE_BA_197_222_R	686	sspE
356	RPLB_EC_650_679_TMOD_F	232	RPLB_EC_739_762_TMOD_R	592	rplB
66	RPLB_EC_650_679_F	231	RPLB_EC_739_762_R	591	rplB
358	VALS_EC_1105_1124_TMOD_F	350	VALS_EC_1195_1218_TMOD_R	712	vals
71	VALS_EC_1105_1124_F	349	VALS_EC_1195_1218_R	711	vals
359	RPOB_EC_1845_1866_TMOD_F	241	RPOB_EC_1909_1929_TMOD_R	597	rpoB
72	RPOB_EC_1845_1866_F	240	RPOB_EC_1909_1929_R	596	rpoB
360	23S_EC_2646_2667_TMOD_F	60	23S_EC_2745_2765_TMOD_R	416	23S rRNA
118	23S_EC_2646_2667_F	59	23S_EC_2745_2765_R	415	23S rRNA
17	23S_EC_2645_2669_F	58	23S_EC_2744_2761_R	414	23S rRNA

361	16S_EC_1090_1111_2_TM0D_F	5	16S_EC_1175_1196_TM0D_R	370	16S rRNA
3	16S_EC_1090_1111_2_F	6	16S_EC_1175_1196_R	369	16S rRNA
362	RPOB_EC_3799_3821_TM0D_F	245	RPOB_EC_3862_3888_TM0D_R	603	rpoB
289	RPOB_EC_3799_3821_F	246	RPOB_EC_3862_3888_R	602	rpoB
363	RPOC_EC_2146_2174_TM0D_F	257	RPOC_EC_2227_2245_TM0D_R	621	rpoC
290	RPOC_EC_2146_2174_F	256	RPOC_EC_2227_2245_R	620	rpoC
367	TUFB_EC_957_979_TM0D_F	345	TUFB_EC_1034_1058_TM0D_R	701	tufB
293	TUFB_EC_957_979_F	344	TUFB_EC_1034_1058_R	700	tufB
449	RPLB_EC_690_710_F	237	RPLB_EC_737_758_R	589	rp1B
357	RPLB_EC_688_710_TM0D_F	236	RPLB_EC_736_757_TM0D_R	588	rp1B
67	RPLB_EC_688_710_F	235	RPLB_EC_736_757_R	587	rp1B

[0117] The 16 primer pairs of the surveillance set are used to produce bioagent identifying amplicons whose base compositions are sufficiently different amongst all known bacteria at the species level to identify, at a reasonable confidence level, any given bacterium at the species level. As shown in Tables 6A-E, common respiratory bacterial pathogens can be distinguished by the base compositions of bioagent identifying amplicons obtained using the 16 primer pairs of the surveillance set. In some cases, triangulation identification improves the confidence level for species assignment. For example, nucleic acid from *Streptococcus pyogenes* can be amplified by nine of the sixteen surveillance primer pairs and *Streptococcus pneumoniae* can be amplified by ten of the sixteen surveillance primer pairs. The base compositions of the bioagent identifying amplicons are identical for only one of the analogous bioagent identifying amplicons and differ in all of the remaining analogous bioagent identifying amplicons by up to four bases per bioagent identifying amplicon. The resolving power of the surveillance set was confirmed by determination of base compositions for 120 isolates of respiratory pathogens representing 70 different bacterial species and the results indicated that natural variations (usually only one or two base substitutions per bioagent identifying amplicon) amongst multiple isolates of the same species did not prevent correct identification of major pathogenic organisms at the species level.

[0118] *Bacillus anthracis* is a well known biological warfare agent which has emerged in domestic terrorism in recent years. Since it was envisioned to produce bioagent identifying amplicons for identification of *Bacillus anthracis*, additional drill-down analysis primers were designed to target genes present on virulence plasmids of *Bacillus anthracis* so that additional confidence could be reached in positive identification of this pathogenic organism. Three drill-down analysis primers were designed and are listed in Tables 1 and 5. In Table 5 the drill-down set comprises primers with T modifications (note TM0D designation in primer names) which

constitutes a functional improvement with regard to prevention of non-templated adenylation (*vide supra*) relative to originally selected primers which are displayed below in the same row.

Table 5: Drill-Down Primer Pairs for Confirmation of Identification of *Bacillus anthracis*

Primer Pair No.	Forward Primer Name	Forward Primer (SEQ ID NO:)	Reverse Primer Name	Reverse Primer (SEQ ID NO:)	Target Gene
350	CAPC_BA_274_303_TM0D_F	98	CAPC_BA_349_376_TM0D_R	452	capC
24	CAPC_BA_274_303_F	97	CAPC_BA_349_376_R	451	capC
351	CYA_BA_1353_1379_TM0D_F	128	CYA_BA_1448_1467_TM0D_R	483	cyA
30	CYA_BA_1353_1379_F	127	CYA_BA_1448_1467_R	482	cyA
353	LEF_BA_756_781_TM0D_F	175	LEF_BA_843_872_TM0D_R	531	lef
37	LEF_BA_756_781_F	174	LEF_BA_843_872_R	530	lef

[0119] Phylogenetic coverage of bacterial space of the sixteen surveillance primers of Table 4 and the three *Bacillus anthracis* drill-down primers of Table 5 is shown in Figure 3 which lists common pathogenic bacteria. Figure 3 is not meant to be comprehensive in illustrating all species identified by the primers. Only pathogenic bacteria are listed as representative examples of the bacterial species that can be identified by the primers and methods of the present invention. Nucleic acid of groups of bacteria enclosed within the polygons of Figure 3 can be amplified to obtain bioagent identifying amplicons using the primer pair numbers listed in the upper right hand corner of each polygon. Primer coverage for polygons within polygons is additive. As an illustrative example, bioagent identifying amplicons can be obtained for *Chlamydia trachomatis* by amplification with, for example, primer pairs 346-349, 360 and 361, but not with any of the remaining primers of the surveillance primer set. On the other hand, bioagent identifying amplicons can be obtained from nucleic acid originating from *Bacillus anthracis* (located within 5 successive polygons) using, for example, any of the following primer pairs: 346-349, 360, 361 (base polygon), 356, 449 (second polygon), 352 (third polygon), 355 (fourth polygon), 350, 351 and 353 (fifth polygon). Multiple coverage of a given organism with multiple primers provides for increased confidence level in identification of the organism as a result of enabling broad triangulation identification.

[0120] In Tables 6A-E, base compositions of respiratory pathogens for primer target regions are shown. Two entries in a cell, represent variation in ribosomal DNA operons. The most predominant base composition is shown first and the minor (frequently a single operon) is indicated by an asterisk (*). Entries with NO DATA mean that the primer would not be expected to prime this species due to mismatches between the primer and target region, as determined by theoretical PCR.

Table 6A – Base Compositions of Common Respiratory Pathogens for Bioagent Identifying Amplicons Corresponding to Primer Pair Nos: 346, 347 and 348

Organism	Strain	Primer 346 [A G C T]	Primer 347 [A G C T]	Primer 348 [A G C T]
<i>Klebsiella pneumoniae</i>	MGH78578	[29 32 25 13] [29 31 25 13]*	[23 38 28 26] [23 37 28 26]*	[26 32 28 30] [26 31 28 30]*
<i>Yersinia pestis</i>	CO-92 Biovar Orientalis	[29 32 25 13]	[22 39 28 26]	[29 30 28 29] [30 30 27 29]*
<i>Yersinia pestis</i>	KIM5 P12 (Biovar Mediavalis)	[29 32 25 13]	[22 39 28 26]	[29 30 28 29] [29 30 28 29] [30 30 27 29]*
<i>Yersinia pestis</i>	91001	[29 32 25 13]	[22 39 28 26]	[29 30 28 29] [30 30 27 29]*
<i>Haemophilus influenzae</i>	KW20	[28 31 23 17]	[24 37 25 27]	[29 30 28 29]
<i>Pseudomonas aeruginosa</i>	PA01	[30 31 23 15]	[26 36 29 24] [27 36 29 23]*	[26 32 29 29]
<i>Pseudomonas fluorescens</i>	Pf0-1	[30 31 23 15]	[26 35 29 25]	[28 31 28 29]
<i>Pseudomonas putida</i>	KT2440	[30 31 23 15]	[28 33 27 27]	[27 32 29 28]
<i>Legionella pneumophila</i>	Philadelphia-1	[30 30 24 15]	[33 33 23 27]	[29 28 28 31]
<i>Francisella tularensis</i>	schu 4	[32 29 22 16]	[28 38 26 26]	[25 32 28 31]
<i>Bordetella pertussis</i>	Tohama I	[30 29 24 16]	[23 37 30 24]	[30 32 30 26]
<i>Burkholderia cepacia</i>	J2315	[29 29 27 14]	[27 32 26 29]	[27 36 31 24] [20 42 35 19]*
<i>Burkholderia pseudomallei</i>	K96243	[29 29 27 14]	[27 32 26 29]	[27 36 31 24]
<i>Neisseria gonorrhoeae</i>	FA 1090, ATCC 700825	[29 28 24 18]	[27 34 26 28]	[24 36 29 27]
<i>Neisseria meningitidis</i>	MC58 (serogroup B)	[29 28 26 16]	[27 34 27 27]	[25 35 30 26]
<i>Neisseria meningitidis</i>	serogroup C, FAM18	[29 28 26 16]	[27 34 27 27]	[25 35 30 26]
<i>Neisseria meningitidis</i>	E2491 (serogroup A)	[29 28 26 16]	[27 34 27 27]	[25 35 30 26]
<i>Chlamydia pneumoniae</i>	TK-183	[31 27 22 19]	NO DATA	[32 27 27 29]
<i>Chlamydia pneumoniae</i>	AR39	[31 27 22 19]	NO DATA	[32 27 27 29]
<i>Chlamydia pneumoniae</i>	CKL029	[31 27 22 19]	NO DATA	[32 27 27 29]
<i>Chlamydia pneumoniae</i>	J138	[31 27 22 19]	NO DATA	[32 27 27 29]
<i>Corynebacterium diphtheriae</i>	NCTC13129	[29 34 21 15]	[22 38 31 25]	[22 33 25 34]
<i>Mycobacterium avium</i>	K10	[27 36 21 15]	[22 37 30 28]	[21 36 27 30]
<i>Mycobacterium avium</i>	104	[27 36 21 15]	[22 37 30 28]	[21 36 27 30]
<i>Mycobacterium tuberculosis</i>	CSU#93	[27 36 21 15]	[22 37 30 28]	[21 36 27 30]
<i>Mycobacterium tuberculosis</i>	CDC 1551	[27 36 21 15]	[22 37 30 28]	[21 36 27 30]
<i>Mycobacterium tuberculosis</i>	H37Rv (lab strain)	[27 36 21 15]	[22 37 30 28]	[21 36 27 30]
<i>Mycoplasma pneumoniae</i>	M129	[31 29 19 20]	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MRSA252	[27 30 21 21]	[25 35 30 26]	[30 29 30 29] [29 31 30 29]*
<i>Staphylococcus aureus</i>	MRSA476	[27 30 21 21]	[25 35 30 26]	[30 29 30 29] [30 29 29 30]*
<i>Staphylococcus aureus</i>	COL	[27 30 21 21]	[25 35 30 26]	[30 29 30 29] [30 29 29 30]*
<i>Staphylococcus aureus</i>	Mu50	[27 30 21 21]	[25 35 30 26]	[30 29 30 29] [30 29 29 30]*
<i>Staphylococcus aureus</i>	MW2	[27 30 21 21]	[25 35 30 26]	[30 29 30 29] [30 29 29 30]*

<i>Staphylococcus aureus</i>	N315	[27 30 21 21]	[25 35 30 26]	[30 29 30 29]
<i>Staphylococcus aureus</i>	NCTC 8325	[27 30 21 21]	[25 35 30 26] [25 35 31 26]*	[30 29 30 29] [30 29 29 30]
<i>Streptococcus agalactiae</i>	NEM316	[26 32 23 18]	[24 36 31 25] [24 36 30 26]*	[25 32 29 30]
<i>Streptococcus equi</i>	NC 002955	[26 32 23 18]	[23 37 31 25]	[29 30 25 32]
<i>Streptococcus pyogenes</i>	MGAS8232	[26 32 23 18]	[24 37 30 25]	[25 31 29 31]
<i>Streptococcus pyogenes</i>	MGAS315	[26 32 23 18]	[24 37 30 25]	[25 31 29 31]
<i>Streptococcus pyogenes</i>	SSI-1	[26 32 23 18]	[24 37 30 25]	[25 31 29 31]
<i>Streptococcus pyogenes</i>	MGAS10394	[26 32 23 18]	[24 37 30 25]	[25 31 29 31]
<i>Streptococcus pyogenes</i>	Manfredo (M5)	[26 32 23 18]	[24 37 30 25]	[25 31 29 31]
<i>Streptococcus pyogenes</i>	SF370 (M1)	[26 32 23 18]	[24 37 30 25]	[25 31 29 31]
<i>Streptococcus pneumoniae</i>	670	[26 32 23 18]	[25 35 28 28]	[25 32 29 30]
<i>Streptococcus pneumoniae</i>	R70	[26 32 23 18]	[25 35 28 28]	[25 32 29 30]
<i>Streptococcus pneumoniae</i>	TIGR4	[26 32 23 18]	[25 35 28 28]	[25 32 30 29]
<i>Streptococcus gordoni</i>	NCTC7868	[25 33 23 18]	[24 36 31 25]	[25 31 29 31]
<i>Streptococcus mitis</i>	NCTC 12261	[26 32 23 18]	[25 35 30 26]	[25 32 29 30] [24 31 35 29]*
<i>Streptococcus mutans</i>	UA159	[24 32 24 19]	[25 37 30 24]	[28 31 26 31]

Table 6B – Base Compositions of Common Respiratory Pathogens for Bioagent Identifying Amplicons Corresponding to Primer Pair Nos: 349, 360, and 356

Organism	Strain	Primer 349 [A G C T]	Primer 360 [A G C T]	Primer 356 [A G C T]
<i>Klebsiella pneumoniae</i>	MGH78578	[25 31 25 22]	[33 37 25 27]	NO DATA
	CO-92 (Biovar Orientalis)	[25 31 27 20] [25 32 26 20]*	[34 35 25 28]	NO DATA
<i>Yersinia pestis</i>	KIM5 P12 (Biovar Mediaevalis)	[25 31 27 20] [25 32 26 20]*	[34 35 25 28]	NO DATA
<i>Yersinia pestis</i>	91001	[25 31 27 20]	[34 35 25 28]	NO DATA
<i>Haemophilus influenzae</i>	KW20	[28 28 25 20]	[32 38 25 27]	NO DATA
<i>Pseudomonas aeruginosa</i>	PAO1	[24 31 26 20]	[31 36 27 27] [31 36 27 28]*	NO DATA
<i>Pseudomonas fluorescens</i>	Pf0-1	NO DATA	[30 37 27 28] [30 37 27 28]	NO DATA
<i>Pseudomonas putida</i>	KT2440	[24 31 26 20]	[30 37 27 28]	NO DATA
<i>Legionella pneumophila</i>	Philadelphia-1	[23 30 25 23]	[30 39 29 24]	NO DATA
<i>Francisella tularensis</i>	schu 4	[26 31 25 19]	[32 36 27 27]	NO DATA
<i>Bordetella pertussis</i>	Tohama I	[21 29 24 18]	[33 36 26 27]	NO DATA
<i>Burkholderia cepacia</i>	J2315	[23 27 22 20]	[31 37 28 26]	NO DATA
<i>Burkholderia pseudomallei</i>	K96243	[23 27 22 20]	[31 37 28 26]	NO DATA
<i>Neisseria gonorrhoeae</i>	FA 1090, ATCC 700825	[24 27 24 17]	[34 37 25 26]	NO DATA
<i>Neisseria meningitidis</i>	MC58 (serogroup B)	[25 27 22 18]	[34 37 25 26]	NO DATA
<i>Neisseria meningitidis</i>	serogroup C, FAM18	[25 26 23 18]	[34 37 25 26]	NO DATA
<i>Neisseria meningitidis</i>	22491 (serogroup A)	[25 26 23 18]	[34 37 25 26]	NO DATA

<i>meningitidis</i>				
<i>Chlamydomonas</i>				
<i>pneumoniae</i>	TW-183	[30 28 27 18]	NO DATA	NO DATA
<i>Chlamydomonas</i>	AR39	[30 28 27 18]	NO DATA	NO DATA
<i>pneumoniae</i>				
<i>Chlamydomonas</i>	CWL029	[30 28 27 18]	NO DATA	NO DATA
<i>pneumoniae</i>				
<i>Chlamydomonas</i>	J138	[30 28 27 18]	NO DATA	NO DATA
<i>pneumoniae</i>				
<i>Corynebacterium</i>	NCTC13129	NO DATA	[29 40 28 25]	NO DATA
<i>diphtheriae</i>				
<i>Mycobacterium</i>	k10	NO DATA	[33 35 32 22]	NO DATA
<i>avium</i>				
<i>Mycobacterium</i>	104	NO DATA	[33 35 32 22]	NO DATA
<i>avium</i>				
<i>Mycobacterium</i>	CSU#93	NO DATA	[30 36 34 22]	NO DATA
<i>tuberculosis</i>				
<i>Mycobacterium</i>	CDC 1551	NO DATA	[30 36 34 22]	NO DATA
<i>tuberculosis</i>				
<i>Mycobacterium</i>	H37Rv (lab strain)	NO DATA	[30 36 34 22]	NO DATA
<i>tuberculosis</i>				
<i>Mycoplasma</i>	M129	[28 30 24 19]	[34 31 29 28]	NO DATA
<i>pneumoniae</i>				
<i>Staphylococcus</i>	MRSa252	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Staphylococcus</i>	MSSA476	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Staphylococcus</i>	COL	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Staphylococcus</i>	Mu50	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Staphylococcus</i>	MW2	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Staphylococcus</i>	N315	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Staphylococcus</i>	NCTC 8325	[26 30 25 20]	[31 38 24 29]	[33 30 31 27]
<i>aureus</i>				
<i>Streptococcus</i>	NEM316	[28 31 22 20]	[33 37 24 28]	[37 30 28 26]
<i>agalactiae</i>				
<i>Streptococcus</i>	NC 002955	[28 31 23 19]	[33 38 24 27]	[37 31 28 25]
<i>equi</i>				
<i>Streptococcus</i>	MGAS8232	[28 31 23 19]	[33 37 24 28]	[38 31 29 23]
<i>pyogenes</i>				
<i>Streptococcus</i>	MGAS315	[28 31 23 19]	[33 37 24 28]	[38 31 29 23]
<i>pyogenes</i>				
<i>Streptococcus</i>	SSI-1	[28 31 23 19]	[33 37 24 28]	[38 31 29 23]
<i>pyogenes</i>				
<i>Streptococcus</i>	MGAS10394	[28 31 23 19]	[33 37 24 28]	[38 31 29 23]
<i>pyogenes</i>				
<i>Streptococcus</i>	Manfredo (M5)	[28 31 23 19]	[33 37 24 28]	[38 31 29 23]
<i>pyogenes</i>				
<i>Streptococcus</i>	SF370 (M1)	[28 31 23 19] [28 31 22 20]*	[33 37 24 28]	[38 31 29 23]
<i>pyogenes</i>				
<i>Streptococcus</i>	670	[28 31 22 20]	[34 36 24 28]	[37 30 29 25]
<i>pneumoniae</i>				
<i>Streptococcus</i>	R6	[28 31 22 20]	[34 36 24 28]	[37 30 29 25]
<i>pneumoniae</i>				
<i>Streptococcus</i>	TIGR4	[28 31 22 20]	[34 36 24 28]	[37 30 29 25]
<i>pneumoniae</i>				
<i>Streptococcus</i>	NCTC7868	[28 32 23 20]	[34 36 24 28]	[36 31 29 25]
<i>gordonii</i>				
<i>Streptococcus</i>	NCTC 12261	[28 31 22 20] [29 30 22 20]*	[34 36 24 28]	[37 30 29 25]
<i>mitis</i>				
<i>Streptococcus</i>	UA159	[26 32 23 22]	[34 37 24 27]	NO DATA
<i>mutans</i>				

Table 6C – Base Compositions of Common Respiratory Pathogens for Bioagent Identifying Amplicons Corresponding to Primer Pair Nos: 449, 354, and 352

Organism	Strain	Primer 449 [A G C T]	Primer 354 [A G C T]	Primer 352 [A G C T]
<i>Klebsiella pneumoniae</i>	MGH78578	NO DATA	[27 33 36 26]	NO DATA
<i>Yersinia pestis</i>	CO-92 Bivvar	NO DATA	[29 31 33 29]	[32 28 20 25]
<i>Yersinia pestis</i>	KIM5 P12 (Bivvar)	NO DATA	[29 31 33 29]	[32 28 20 25]
<i>Yersinia pestis</i>	91001	NO DATA	[29 31 33 29]	NO DATA
<i>Haemophilus influenzae</i>	KW20	NO DATA	[30 29 31 32]	NO DATA
<i>Pseudomonas aeruginosa</i>	PAO1	NO DATA	[26 33 39 24]	NO DATA
<i>Pseudomonas fluorescens</i>	Pf0-1	NO DATA	[26 33 34 29]	NO DATA
<i>Pseudomonas putida</i>	KT2440	NO DATA	[25 34 36 27]	NO DATA
<i>Legionella pneumophila</i>	Philadelphia-1	NO DATA	NO DATA	NO DATA
<i>Francisella tularensis</i>	schu 4	NO DATA	[33 32 25 32]	NO DATA
<i>Bordetella pertussis</i>	Tohama I	NO DATA	[26 33 39 24]	NO DATA
<i>Burkholderia cepacia</i>	J2315	NO DATA	[25 37 33 27]	NO DATA
<i>Burkholderia pseudomallei</i>	K96243	NO DATA	[25 37 34 26]	NO DATA
<i>Neisseria gonorrhoeae</i>	FA 1090, ATCC 700825	[17 23 22 10]	[29 31 32 30]	NO DATA
<i>Neisseria meningitidis</i>	MC58 (serogroup B)	NO DATA	[29 30 32 31]	NO DATA
<i>Neisseria meningitidis</i>	serogroup C, FAM18	NO DATA	[29 30 32 31]	NO DATA
<i>Neisseria meningitidis</i>	Z2491 (serogroup A)	NO DATA	[29 30 32 31]	NO DATA
<i>Chlamydia pneumoniae</i>	TW-183	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	AR39	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	CWL029	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	J138	NO DATA	NO DATA	NO DATA
<i>Corynebacterium diphtheriae</i>	NCTC13129	NO DATA	NO DATA	NO DATA
<i>Mycobacterium avium</i>	k10	NO DATA	NO DATA	NO DATA
<i>Mycobacterium avium</i>	104	NO DATA	NO DATA	NO DATA
<i>Mycobacterium tuberculosis</i>	CSU#93	NO DATA	NO DATA	NO DATA
<i>Mycobacterium tuberculosis</i>	CDC 1551	NO DATA	NO DATA	NO DATA
<i>Mycobacterium tuberculosis</i>	H37Rv (lab strain)	NO DATA	NO DATA	NO DATA
<i>Mycoplasma pneumoniae</i>	M129	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MRSA252	[17 20 21 17]	[30 27 30 35]	[36 24 19 26]
<i>Staphylococcus aureus</i>	MSSA476	[17 20 21 17]	[30 27 30 35]	[36 24 19 26]
<i>Staphylococcus aureus</i>	COL	[17 20 21 17]	[30 27 30 35]	[35 24 19 27]
<i>Staphylococcus aureus</i>	Mu50	[17 20 21 17]	[30 27 30 35]	[36 24 19 26]
<i>Staphylococcus aureus</i>	MW2	[17 20 21 17]	[30 27 30 35]	[36 24 19 26]

<i>Staphylococcus aureus</i>	N315	[17 20 21 17]	[30 27 30 35]	[36 24 19 26]
<i>Staphylococcus aureus</i>	NCTC 8325	[17 20 21 17]	[30 27 30 35]	[35 24 19 27]
<i>Streptococcus agalactiae</i>	NEM316	[22 20 19 14]	[26 31 27 38]	[29 26 22 28]
<i>Streptococcus equi</i>	MC 002955	[22 21 19 13]	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	NGAS8232	[23 21 19 12]	[24 32 30 36]	NO DATA
<i>Streptococcus pyogenes</i>	NGAS315	[23 21 19 12]	[24 32 30 36]	NO DATA
<i>Streptococcus pyogenes</i>	SSI-1	[23 21 19 12]	[24 32 30 36]	NO DATA
<i>Streptococcus pyogenes</i>	NGAS10394	[23 21 19 12]	[24 32 30 36]	NO DATA
<i>Streptococcus pyogenes</i>	Manfredo (M5)	[23 21 19 12]	[24 32 30 36]	NO DATA
<i>Streptococcus pyogenes</i>	SF370 (M1)	[23 21 19 12]	[24 32 30 36]	NO DATA
<i>Streptococcus pneumoniae</i>	670	[22 20 19 14]	[25 33 29 35]	[30 29 21 25]
<i>Streptococcus pneumoniae</i>	R6	[22 20 19 14]	[25 33 29 35]	[30 29 21 25]
<i>Streptococcus pneumoniae</i>	TIGR4	[22 20 19 14]	[25 33 29 35]	[30 29 21 25]
<i>Streptococcus gordonii</i>	NCTC7868	[21 21 19 14]	NO DATA	[29 26 22 28]
<i>Streptococcus mitis</i>	NCTC 12261	[22 20 19 14]	[26 30 32 34]	NO DATA
<i>Streptococcus mutans</i>	UA159	NO DATA	NO DATA	NO DATA

Table 6D – Base Compositions of Common Respiratory Pathogens for Bioagent Identifying Amplicons Corresponding to Primer Pair Nos: 355, 358, and 359

Organism	Strain	Primer 355 [A G C T]	Primer 358 [A G C T]	Primer 359 [A G C T]
<i>Klebsiella pneumoniae</i>	MGH78578	NO DATA	[24 39 33 20]	[25 21 24 17]
<i>Yersinia pestis</i>	CO-92 (Biovar Orientalis)	NO DATA	[26 34 35 21]	[23 23 19 22]
<i>Yersinia pestis</i>	KIM5 Fl2 (Biovar Mediaevalis)	NO DATA	[26 34 35 21]	[23 23 19 22]
<i>Yersinia pestis</i>	91001	NO DATA	[26 34 35 21]	[23 23 19 22]
<i>Haemophilus influenzae</i>	KW20	NO DATA	NO DATA	NO DATA
<i>Pseudomonas aeruginosa</i>	PA01	NO DATA	NO DATA	NO DATA
<i>Pseudomonas fluorescens</i>	Pf0-1	NO DATA	NO DATA	NO DATA
<i>Pseudomonas putida</i>	KT2440	NO DATA	[21 37 37 21]	NO DATA
<i>Legionella pneumophila</i>	Philadelphia-1	NO DATA	NO DATA	NO DATA
<i>Francisella tularensis</i>	schu 4	NO DATA	NO DATA	NO DATA
<i>Bordetella pertussis</i>	Tohame I	NO DATA	NO DATA	NO DATA
<i>Burkholderia cepacia</i>	J2315	NO DATA	NO DATA	NO DATA
<i>Burkholderia pseudomallei</i>	K96243	NO DATA	NO DATA	NO DATA
<i>Neisseria gonorrhoeae</i>	FA 1090, ATCC 700825	NO DATA	NO DATA	NO DATA
<i>Neisseria meningitidis</i>	MC59 (serogroup B)	NO DATA	NO DATA	NO DATA
<i>Neisseria meningitidis</i>	serogroup C, FAM18	NO DATA	NO DATA	NO DATA

<i>Neisseria meningitidis</i>	Z2491 (serogroup A)	NO DATA	NO DATA	NO DATA
<i>Chlamydomonas pneumoniae</i>	TW-183	NO DATA	NO DATA	NO DATA
<i>Chlamydomonas pneumoniae</i>	AR39	NO DATA	NO DATA	NO DATA
<i>Chlamydomonas pneumoniae</i>	CWL029	NO DATA	NO DATA	NO DATA
<i>Chlamydomonas pneumoniae</i>	J138	NO DATA	NO DATA	NO DATA
<i>Corynebacterium diphtheriae</i>	NCTC13129	NO DATA	NO DATA	NO DATA
<i>Mycobacterium avium</i>	k10	NO DATA	NO DATA	NO DATA
<i>Mycobacterium avium</i>	104	NO DATA	NO DATA	NO DATA
<i>Mycobacterium tuberculosis</i>	CSU#93	NO DATA	NO DATA	NO DATA
<i>Mycobacterium tuberculosis</i>	CDC 1551	NO DATA	NO DATA	NO DATA
<i>Mycobacterium tuberculosis</i>	H37Rv (lab strain)	NO DATA	NO DATA	NO DATA
<i>Mycoplasma pneumoniae</i>	M129	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MRSA252	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MSEA476	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	COL	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	Mu50	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MW2	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	N315	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	NCTC 8325	NO DATA	NO DATA	NO DATA
<i>Streptococcus agalactiae</i>	NEM316	NO DATA	NO DATA	NO DATA
<i>Streptococcus equi</i>	NC 002955	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	MGAS8232	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	MGAS315	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	SS1-1	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	MGAS10394	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	Manfredo (M5)	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	SF370 (M1)	NO DATA	NO DATA	NO DATA
<i>Streptococcus pneumoniae</i>	670	NO DATA	NO DATA	NO DATA
<i>Streptococcus pneumoniae</i>	R6	NO DATA	NO DATA	NO DATA
<i>Streptococcus pneumoniae</i>	TIGR4	NO DATA	NO DATA	NO DATA
<i>Streptococcus gordoni</i>	NCTC7868	NO DATA	NO DATA	NO DATA
<i>Streptococcus mitis</i>	NCTC 12261	NO DATA	NO DATA	NO DATA
<i>Streptococcus mutans</i>	UA159	NO DATA	NO DATA	NO DATA

Table 6E – Base Compositions of Common Respiratory Pathogens for Bioagent Identifying Amplicons Corresponding to Primer Pair Nos: 362, 363, and 367

Organism	Strain	Primer 362 [A G C T]	Primer 363 [A G C T]	Primer 367 [A G C T]
<i>Klebsiella pneumoniae</i>	MGH78578	[21 33 22 16]	[16 34 26 26]	NO DATA
<i>Yersinia pestis</i>	CO-92 Orientalis (Biovar)	[20 34 18 20]	NO DATA	NO DATA
<i>Yersinia pestis</i>	KIM5 P12 Mediaevalis (Biovar)	[20 34 18 20]	NO DATA	NO DATA
<i>Yersinia pestis</i>	91001	[20 34 18 20]	NO DATA	NO DATA
<i>Haemophilus influenzae</i>	KW20	NO DATA	NO DATA	NO DATA
<i>Pseudomonas aeruginosa</i>	PAO1	[19 35 21 17]	[16 36 28 22]	NO DATA
<i>Pseudomonas fluorescens</i>	Pf0-1	NO DATA	[18 35 26 23]	NO DATA
<i>Pseudomonas putida</i>	KT2440	NO DATA	[16 35 28 23]	NO DATA
<i>Legionella pneumophila</i>	Philadelphia-1	NO DATA	NO DATA	NO DATA
<i>Francisella tularensis</i>	schu 4	NO DATA	NO DATA	NO DATA
<i>Bordetella pertussis</i>	Tohama I	[20 31 24 17]	[15 34 32 21]	[26 25 34 19]
<i>Burkholderia cepacia</i>	J2315	[20 33 21 18]	[15 36 26 25]	[25 27 32 20]
<i>Burkholderia pseudomallei</i>	K96243	[19 34 19 20]	[15 37 28 22]	[25 27 32 20]
<i>Neisseria gonorrhoeae</i>	FA 1090, ATCC 700825	NO DATA	NO DATA	NO DATA
<i>Neisseria meningitidis</i>	MC58 (serogroup B)	NO DATA	NO DATA	NO DATA
<i>Neisseria meningitidis</i>	serogroup C, FAM18	NO DATA	NO DATA	NO DATA
<i>Neisseria meningitidis</i>	Z2491 (serogroup A)	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	TW-183	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	AR39	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	CWL029	NO DATA	NO DATA	NO DATA
<i>Chlamydia pneumoniae</i>	J138	NO DATA	NO DATA	NO DATA
<i>Corynebacterium diphtheriae</i>	NCTC13129	NO DATA	NO DATA	NO DATA
<i>Mycobacterium avium</i>	k10	[19 34 23 16]	NO DATA	[24 26 35 19]
<i>Mycobacterium avium</i>	104	[19 34 23 16]	NO DATA	[24 26 35 19]
<i>Mycobacterium tuberculosis</i>	CSU#93	[19 31 25 17]	NO DATA	[25 25 34 20]
<i>Mycobacterium tuberculosis</i>	CDC 1551	[19 31 24 18]	NO DATA	[25 25 34 20]
<i>Mycobacterium tuberculosis</i>	H37Rv (lab strain)	[19 31 24 18]	NO DATA	[25 25 34 20]
<i>Mycoplasma pneumoniae</i>	M129	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MSSA252	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MSSA476	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	COL	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	M150	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	MW2	NO DATA	NO DATA	NO DATA
<i>Staphylococcus aureus</i>	N315	NO DATA	NO DATA	NO DATA

<i>aureus</i>				
<i>Staphylococcus aureus</i>	NCTC 8325	NO DATA	NO DATA	NO DATA
<i>Streptococcus agalactiae</i>	NEM316	NO DATA	NO DATA	NO DATA
<i>Streptococcus equi</i>	NC 002955	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	MGAS8232	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	MGAS315	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	SSI-1	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	MGAS10394	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	Manfredo (M5)	NO DATA	NO DATA	NO DATA
<i>Streptococcus pyogenes</i>	SF370 (M1)	NO DATA	NO DATA	NO DATA
<i>Streptococcus pneumoniae</i>	670	NO DATA	NO DATA	NO DATA
<i>Streptococcus pneumoniae</i>	R6	[20 30 19 23]	NO DATA	NO DATA
<i>Streptococcus pneumoniae</i>	TIGR4	[20 30 19 23]	NO DATA	NO DATA
<i>Streptococcus gordonii</i>	NCTC786B	NO DATA	NO DATA	NO DATA
<i>Streptococcus mitis</i>	NCTC 12261	NO DATA	NO DATA	NO DATA
<i>Streptococcus mutans</i>	UA159	NO DATA	NO DATA	NO DATA

[0121] Four sets of throat samples from military recruits at different military facilities taken at different time points were analyzed using the primers of the present invention. The first set was collected at a military training center from November 1 to December 20, 2002 during one of the most severe outbreaks of pneumonia associated with group A *Streptococcus* in the United States since 1968. During this outbreak, fifty-one throat swabs were taken from both healthy and hospitalized recruits and plated on blood agar for selection of putative group A *Streptococcus* colonies. A second set of 15 original patient specimens was taken during the height of this group A *Streptococcus*-associated respiratory disease outbreak. The third set were historical samples, including twenty-seven isolates of group A *Streptococcus*, from disease outbreaks at this and other military training facilities during previous years. The fourth set of samples was collected from five geographically separated military facilities in the continental U.S. in the winter immediately following the severe November/December 2002 outbreak.

[0122] Pure colonies isolated from group A *Streptococcus*-selective media from all four collection periods were analyzed with the surveillance primer set. All samples showed base compositions that precisely matched the four completely sequenced strains of *Streptococcus pyogenes*. Shown in Figure 4 is a 3D diagram of base composition (axes A, G and C) of bioagent identifying amplicons obtained with primer pair number 14 (a precursor of primer pair

number 348 which targets 16S rRNA). The diagram indicates that the experimentally determined base compositions of the clinical samples closely match the base compositions expected for *Streptococcus pyogenes* and are distinct from the expected base compositions of other organisms.

[0123] In addition to the identification of *Streptococcus pyogenes*, other potentially pathogenic organisms were identified concurrently. Mass spectral analysis of a sample whose nucleic acid was amplified by primer pair number 349 (SEQ ID NOs: 49 and 405) exhibited signals of bioagent identifying amplicons with molecular masses that were found to correspond to analogous base compositions of bioagent identifying amplicons of *Streptococcus pyogenes* (A27 G32 C24 T18), *Neisseria meningitidis* (A25 G37 C22 T18), and *Haemophilus influenzae* (A28 G28 C25 T20) (see Figure 5 and Table 6B). These organisms were present in a ratio of 4:5:20 as determined by comparison of peak heights with peak height of an internal PCR calibration standard as described in commonly owned U. S. Patent Application Serial No: 60/545,425 which is incorporated herein by reference in its entirety.

[0124] Since certain division-wide primers that target housekeeping genes are designed to provide coverage of specific divisions of bacteria to increase the confidence level for identification of bacterial species, they are not expected to yield bioagent identifying amplicons for organisms outside of the specific divisions. For example, primer pair number 356 (SEQ ID NOs: 232:592) primarily amplifies the nucleic acid of members of the classes *Bacilli* and *Clostridia* and is not expected to amplify proteobacteria such as *Neisseria meningitidis* and *Haemophilus influenzae*. As expected, analysis of the mass spectrum of amplification products obtained with primer pair number 356 does not indicate the presence of *Neisseria meningitidis* and *Haemophilus influenzae* but does indicate the presence of *Streptococcus pyogenes* (Figures 3 and 6, Table 6B). Thus, these primers or types of primers can confirm the absence of particular bioagents from a sample.

[0125] The 15 throat swabs from military recruits were found to contain a relatively small set of microbes in high abundance. The most common were *Haemophilus influenzae*, *Neisseria meningitidis*, and *Streptococcus pyogenes*. *Staphylococcus epidermidis*, *Moraxella catarrhalis*, *Corynebacterium pseudodiphtheriticum*, and *Staphylococcus aureus* were present in fewer samples. An equal number of samples from healthy volunteers from three different geographic locations, were identically analyzed. Results indicated that the healthy volunteers have bacterial

flora dominated by multiple, commensal non-beta-hemolytic *Streptococcal* species, including the viridans group streptococci (*S. parasanguis*, *S. vestibularis*, *S. mitis*, *S. oralis* and *S. pneumoniae*; data not shown), and none of the organisms found in the military recruits were found in the healthy controls at concentrations detectable by mass spectrometry. Thus, the military recruits in the midst of a respiratory disease outbreak had a dramatically different microbial population than that experienced by the general population in the absence of epidemic disease.

[0126] Example 8: Drill-down Analysis for Determination of *emm*-Type of *Streptococcus pyogenes* in Epidemic Surveillance

[0127] As a continuation of the epidemic surveillance investigation of Example 7, determination of sub-species characteristics (genotyping) of *Streptococcus pyogenes*, was carried out based on a strategy that generates strain-specific signatures according to the rationale of Multi-Locus Sequence Typing (MLST). In classic MLST analysis, internal fragments of several housekeeping genes are amplified and sequenced (Enright et al. *Infection and Immunity*, 2001, 69, 2416-2427). In classic MLST analysis, internal fragments of several housekeeping genes are amplified and sequenced. In the present investigation, bioagent identifying amplicons from housekeeping genes were produced using drill-down primers and analyzed by mass spectrometry. Since mass spectral analysis results in molecular mass, from which base composition can be determined, the challenge was to determine whether resolution of *emm* classification of strains of *Streptococcus pyogenes* could be determined.

[0128] An alignment was constructed of concatenated alleles of seven MLST housekeeping genes (glucose kinase (*gki*), glutamine transporter protein (*gtr*), glutamate racemase (*murI*), DNA mismatch repair protein (*mutS*), xanthine phosphoribosyl transferase (*xpt*), and acetyl-CoA acetyl transferase (*yqiL*)) from each of the 212 previously *emm*-typed strains of *Streptococcus pyogenes*. From this alignment, the number and location of primer pairs that would maximize strain identification via base composition was determined. As a result, 6 primer pairs were chosen as standard drill-down primers for determination of *emm*-type of *Streptococcus pyogenes*. These six primer pairs are displayed in Table 7. This drill-down set comprises primers with T modifications (note TMOD designation in primer names) which constitutes a functional improvement with regard to prevention of non-templated adenylation (*vide supra*) relative to originally selected primers which are displayed below in the same row.

Table 7: Group A *Streptococcus* Drill-Down Primer Pairs

Primer Pair No.	Forward Primer Name	Forward Primer (SEQ ID NO:)	Reverse Primer Name	Reverse Primer (SEQ ID NO:)	Target Gene
442	SP101_SPET11_358_367_TMOD_F	311	SP101_SPET11_448_473_TMOD_R	669	gki
80	SP101_SPET11_358_367_F	310	SP101_SPET11_448_473_TMOD_R	668	gki
443	SP101_SPET11_600_629_TMOD_F	314	SP101_SPET11_686_714_TMOD_R	671	gtr
81	SP101_SPET11_600_629_F	313	SP101_SPET11_686_714_R	670	gtr
426	SP101_SPET11_1314_1336_TMOD_F	278	SP101_SPET11_1403_1431_TMOD_R	633	murI
86	SP101_SPET11_1314_1336_F	277	SP101_SPET11_1403_1431_R	632	murI
430	SP101_SPET11_1807_1835_TMOD_F	286	SP101_SPET11_1901_1927_TMOD_R	641	matS
90	SP101_SPET11_1807_1835_F	285	SP101_SPET11_1901_1927_R	640	matS
438	SP101_SPET11_3075_3103_TMOD_F	302	SP101_SPET11_3168_3196_TMOD_R	657	xpt
96	SP101_SPET11_3075_3103_F	301	SP101_SPET11_3168_3196_R	656	xpt
441	SP101_SPET11_3511_3535_TMOD_F	309	SP101_SPET11_3605_3629_TMOD_R	664	yqiL
98	SP101_SPET11_3511_3535_F	308	SP101_SPET11_3605_3629_R	663	yqiL

[0129] The primers of Table 7 were used to produce bioagent identifying amplicons from nucleic acid present in the clinical samples. The bioagent identifying amplicons which were subsequently analyzed by mass spectrometry and base compositions corresponding to the molecular masses were calculated.

[0130] Of the 51 samples taken during the peak of the November/December 2002 epidemic (Table 8A-C rows 1-3), all except three samples were found to represent *emm*3, a Group A *Streptococcus* genotype previously associated with high respiratory virulence. The three outliers were from samples obtained from healthy individuals and probably represent non-epidemic strains. Archived samples (Tables 8A-C rows 5-13) from historical collections showed a greater heterogeneity of base compositions and *emm* types as would be expected from different epidemics occurring at different places and dates. The results of the mass spectrometry analysis and *emm* gene sequencing were found to be concordant for the epidemic and historical samples.

Table 8A: Base Composition Analysis of Bioagent Identifying Amplicons of Group A *Streptococcus* samples from Six Military Installations Obtained with Primer Pair Nos. 426 and 430

# of Instances	emm-type by Mass Spectrometry	emm-Gene Sequencing	Location (sample)	Year	murI (Primer Pair No. 426)	mutS (Primer Pair No. 430)
48	3	3	MCRD San Diego (Cultured)	2002	A39 G25 C20 T34	A38 G27 C23 T33
2	6	6			A40 G24 C20 T34	A38 G27 C23 T33
1	28	28			A39 G25 C20 T34	A38 G27 C23 T33
15	3	ND			A39 G25 C20 T34	A38 G27 C23 T33
6	3	3	NHRCD San Diego-Archive (Cultured)	2003	A39 G25 C20 T34	A38 G27 C23 T33
3	5,58	5			A40 G24 C20 T34	A38 G27 C23 T33
6	6	6			A40 G24 C20 T34	A38 G27 C23 T33
1	11	11			A39 G25 C20 T34	A38 G27 C23 T33
3	12	12			A40 G24 C20 T34	A38 G26 C24 T33
1	22	22			A39 G25 C20 T34	A38 G27 C23 T33
3	25,75	75			A39 G25 C20 T34	A38 G27 C23 T33
4	44/61, 82, 9	44/61			A40 G24 C20 T34	A38 G26 C24 T33
2	53, 91	91			A39 G25 C20 T34	A38 G27 C23 T33
1	2	2			A39 G25 C20 T34	A38 G27 C24 T32
2	3	3	Ft. Leonard Wood (Cultured)	2003	A39 G25 C20 T34	A38 G27 C23 T33
1	4	4			A39 G25 C20 T34	A38 G27 C23 T33
1	6	6			A40 G24 C20 T34	A38 G27 C23 T33
11	25 or 75	75			A39 G25 C20 T34	A38 G27 C23 T33
1	25, 75, 33, 34, 4, 52, 84	75			A39 G25 C20 T34	A38 G27 C23 T33
1	44/61 or 82 or 9	44/61			A40 G24 C20 T34	A38 G26 C24 T33
2	5 or 58	5			A40 G24 C20 T34	A38 G27 C23 T33
3	1	1			A40 G24 C20 T34	A38 G27 C23 T33
2	3	3			A39 G25 C20 T34	A38 G27 C23 T33
1	4	4			A39 G25 C20 T34	A38 G27 C23 T33
1	28	28	Ft. Sill (Cultured)	2003	A39 G25 C20 T34	A38 G27 C23 T33
1	3	3			A39 G25 C20 T34	A38 G27 C23 T33
1	4	4			A39 G25 C20 T34	A38 G27 C23 T33
3	6	6			A40 G24 C20 T34	A38 G27 C23 T33
1	11	11			A39 G25 C20 T34	A38 G27 C23 T33
1	13	94**			A40 G24 C20 T34	A38 G27 C23 T33
1	44/61 or 82 or 9	82			A40 G24 C20 T34	A38 G26 C24 T33
1	5 or 58	58			A40 G24 C20 T34	A38 G27 C23 T33
1	78 or 89	89			A39 G25 C20 T34	A38 G27 C23 T33
2	5 or 58				A40 G24 C20 T34	A38 G27 C23 T33
1	2	ND	Lackland AFB (Throat Swabs)	2003	A39 G25 C20 T34	A38 G27 C24 T32
1	81 or 90				A40 G24 C20 T34	A38 G27 C23 T33
1	78				A38 G26 C20 T34	A38 G27 C23 T33
3***	No detection				No detection	No detection
7	3	ND	MCRD San Diego (Throat Swabs)	2002	A39 G25 C20 T34	A38 G27 C23 T33
1	3	ND			No detection	A38 G27 C23 T33
1	3	ND			No detection	No detection
1	3	ND			No detection	No detection
2	3	ND			No detection	A38 G27 C23 T33
3	No detection	ND			No detection	No detection

Table 8B: Base Composition Analysis of Bioagent Identifying Amplicons of Group A *Streptococcus* samples from Six Military Installations Obtained with Primer Pair Nos. 438 and 441

# of Instances	emm-type by Mass Spectrometry	emm-Gene Sequencing	Location (sample)	Year	xpt (Primer Pair No. 438)	yqIL (Primer Pair No. 441)	
48	3	3	MCRD San Diego (Cultured)	2002	A30 G36 C20 T36	A40 G29 C19 T31	
2	6	6			A30 G36 C20 T36	A40 G29 C19 T31	
1	28	28			A30 G36 C20 T36	A41 G28 C18 T32	
15	3	ND			A30 G36 C20 T36	A40 G29 C19 T31	
6	3	3	NHRC San Diego-Archive (Cultured)	2003	A30 G36 C20 T36	A40 G29 C19 T31	
3	5,58	5			A30 G36 C20 T36	A40 G29 C19 T31	
6	6	6			A30 G36 C20 T36	A40 G29 C19 T31	
1	11	11			A30 G36 C20 T36	A40 G29 C19 T31	
3	12	12			A30 G36 C19 T37	A40 G29 C19 T31	
1	22	22			A30 G36 C20 T36	A40 G29 C19 T31	
3	25,75	75			A30 G36 C20 T36	A40 G29 C19 T31	
4	44/61,82,9	44/61			A30 G36 C20 T36	A41 G28 C19 T31	
2	53,91	91			A30 G36 C19 T37	A40 G29 C19 T31	
1	2	2			A30 G36 C20 T36	A40 G29 C19 T31	
2	3	3	Ft. Leonard Wood (Cultured)	2003	A30 G36 C20 T36	A40 G29 C19 T31	
1	4	4			A30 G36 C19 T37	A41 G28 C19 T31	
1	6	6			A30 G36 C20 T36	A40 G29 C19 T31	
11	25 or 75	75			A30 G36 C20 T36	A40 G29 C19 T31	
1	25,75, 33, 34,4,52,84	75			A30 G36 C19 T37	A40 G29 C19 T31	
1	44/61 or 82 or 9	44/61			A30 G36 C20 T36	A41 G28 C19 T31	
2	5 or 58	5			A30 G36 C20 T36	A40 G29 C19 T31	
3	1	1			A30 G36 C19 T37	A40 G29 C19 T31	
2	3	3			A30 G36 C20 T36	A40 G29 C19 T31	
1	4	4			A30 G36 C19 T37	A41 G28 C19 T31	
1	28	28	Ft. Benning (Cultured)	2003	A30 G36 C20 T36	A41 G28 C18 T32	
1	3	3			A30 G36 C20 T36	A40 G29 C19 T31	
1	4	4			A30 G36 C19 T37	A41 G28 C19 T31	
3	6	6			A30 G36 C20 T36	A40 G29 C19 T31	
1	11	11			A30 G36 C20 T36	A40 G29 C19 T31	
1	13	94**			A30 G36 C20 T36	A41 G28 C19 T31	
1	44/61 or 82 or 9	82			A30 G36 C20 T36	A41 G28 C19 T31	
1	5 or 58	58			A30 G36 C20 T36	A40 G29 C19 T31	
1	78 or 89	89			A30 G36 C20 T36	A41 G28 C19 T31	
2	5 or 58	ND			A30 G36 C20 T36	A40 G29 C19 T31	
1	2		A30 G36 C20 T36	A40 G29 C19 T31			
1	81 or 90		A30 G36 C20 T36	A40 G29 C19 T31			
1	78		A30 G36 C20 T36	A41 G28 C19 T31			
3***	No detection		No detection	No detection			
7	3		ND	MCRD San Diego (Throat Swabs)	2002	A30 G36 C20 T36	A40 G29 C19 T31
1	3		ND			A30 G36 C20 T36	A40 G29 C19 T31
1	3		ND			A30 G36 C20 T36	No detection
1	3		ND			No detection	A40 G29 C19 T31
2	3		ND			A30 G36 C20 T36	A40 G29 C19 T31
3	No detection	ND	No detection			No detection	

Table 8C: Base Composition Analysis of Bioagent Identifying Amplicons of Group A *Streptococcus* samples from Six Military Installations Obtained with Primer Pair Nos. 438 and 441

# of Instances	emm-type by Mass Spectrometry	emm-Gene Sequencing	Location (sample)	Year	gki (Primer Pair No. 442)	gtr (Primer Pair No. 443)
48	3	3	MCRD San Diego (Cultured)	2002	A32 G35 C17 T32	A39 G28 C16 T32
2	6	6			A31 G35 C17 T33	A39 G28 C15 T33
1	28	28			A30 G36 C17 T33	A39 G28 C16 T32
15	3	ND			A32 G35 C17 T32	A39 G28 C16 T32
6	3	3	NHRC San Diego-Archive (Cultured)	2003	A32 G35 C17 T32	A39 G28 C16 T32
3	5,58	5			A30 G36 C20 T30	A39 G28 C15 T33
6	6	6			A31 G35 C17 T33	A39 G28 C15 T33
1	11	11			A30 G36 C20 T30	A39 G28 C16 T32
3	12	12			A31 G35 C17 T33	A39 G28 C15 T33
3	22	22			A31 G35 C17 T33	A38 G29 C15 T33
3	25,75	75			A30 G36 C17 T33	A39 G28 C15 T33
4	44/61,82,9	44/61			A30 G36 C18 T32	A39 G28 C15 T33
2	53,91	91			A32 G35 C17 T32	A39 G28 C16 T32
1	2	2	Ft. Leonard Wood (Cultured)	2003	A30 G36 C17 T33	A39 G28 C15 T33
2	3	3			A32 G35 C17 T32	A39 G28 C16 T32
1	4	4			A31 G35 C17 T33	A39 G28 C15 T33
1	6	6			A31 G35 C17 T33	A39 G28 C15 T33
11	25 or 75	75			A30 G36 C17 T33	A39 G28 C15 T33
1	25,75, 33, 34,4,52,84	75			A30 G36 C17 T33	A39 G28 C15 T33
1	44/61 or 82 or 9	44/61			A30 G36 C18 T32	A39 G28 C15 T33
2	5 or 58	5			A30 G36 C20 T30	A39 G28 C15 T33
3	1	1			A30 G36 C18 T32	A39 G28 C15 T33
2	3	3	Ft. Sill (Cultured)	2003	A32 G35 C17 T32	A39 G28 C16 T32
1	4	4			A31 G35 C17 T33	A39 G28 C15 T33
1	28	28			A30 G36 C17 T33	A39 G28 C16 T32
1	3	3			A32 G35 C17 T32	A39 G28 C16 T32
1	4	4	Ft. Benning (Cultured)	2003	A31 G35 C17 T33	A39 G28 C15 T33
3	6	6			A31 G35 C17 T33	A39 G28 C15 T33
1	11	11			A30 G36 C20 T30	A39 G28 C16 T32
1	13	94**			A30 G36 C19 T31	A39 G28 C15 T33
1	44/61 or 82 or 9	82			A30 G36 C18 T32	A39 G28 C15 T33
1	5 or 58	58			A30 G36 C20 T30	A39 G28 C15 T33
1	78 or 89	89			A30 G36 C18 T32	A39 G28 C15 T33
2	5 or 58				A30 G36 C20 T30	A39 G28 C15 T33
1	2				A30 G36 C17 T33	A39 G28 C15 T33
1	81 or 90	ND			A30 G36 C17 T33	A39 G28 C15 T33
1	78		Lackland AFB (Throat Swabs)	2003	A30 G36 C18 T32	A39 G28 C15 T33
3***	No detection				No detection	No detection
7	3	ND			A32 G35 C17 T32	A39 G28 C16 T32
1	3	ND			No detection	No detection
1	3	ND	MCRD San Diego (Throat Swabs)	2002	A32 G35 C17 T32	A39 G28 C16 T32
1	3	ND			A32 G35 C17 T32	No detection
2	3	ND			A32 G35 C17 T32	No detection
3	No detection	ND			No detection	No detection

[0131] Example 9: Design of Calibrant Polynucleotides based on Bioagent Identifying Amplicons for Identification of Species of Bacteria (Bacterial Bioagent Identifying Amplicons)

[0132] This example describes the design of 19 calibrant polynucleotides based on bacterial bioagent identifying amplicons corresponding to the primers of the broad surveillance set (Table 4) and the *Bacillus anthracis* drill-down set (Table 5).

[0133] Calibration sequences were designed to simulate bacterial bioagent identifying amplicons produced by the T modified primer pairs shown in Table 4 (primer names have the designation "TMOD"). The calibration sequences were chosen as a representative member of the section of bacterial genome from specific bacterial species which would be amplified by a given primer pair. The model bacterial species upon which the calibration sequences are based are also shown in Table 9. For example, the calibration sequence chosen to correspond to an amplicon produced by primer pair no. 361 is SEQ ID NO: 722. In Table 9, the forward (_F) or reverse (_R) primer name indicates the coordinates of an extraction representing a gene of a standard reference bacterial genome to which the primer hybridizes e.g.: the forward primer name 16S_EC_713_732_TMODO_F indicates that the forward primer hybridizes to residues 713-732 of the gene encoding 16S ribosomal RNA in an *E. coli* reference sequence (in this case, the reference sequence is an extraction consisting of residues 4033120-4034661 of the genomic sequence of *E. coli* K12 (GenBank gi number 16127994). Additional gene coordinate reference information is shown in Table 10. The designation "TMOD" in the primer names indicates that the 5' end of the primer has been modified with a non-matched template T residue which prevents the PCR polymerase from adding non-templated adenosine residues to the 5' end of the amplification product, an occurrence which may result in miscalculation of base composition from molecular mass data (*vide supra*).

[0134] The 19 calibration sequences described in Tables 9 and 10 were combined into a single calibration polynucleotide sequence (SEQ ID NO: 741 - which is herein designated a "combination calibration polynucleotide") which was then cloned into a pCR®-Blunt vector (Invitrogen, Carlsbad, CA). This combination calibration polynucleotide can be used in conjunction with the primers of Table 9 as an internal standard to produce calibration amplicons for use in determination of the quantity of any bacterial bioagent. Thus, for example, when the combination calibration polynucleotide vector is present in an amplification reaction mixture, a calibration amplicon based on primer pair 346 (16S rRNA) will be produced in an amplification

reaction with primer pair 346 and a calibration amplicon based on primer pair 363 (rpoC) will be produced with primer pair 363. Coordinates of each of the 19 calibration sequences within the calibration polynucleotide (SEQ ID NO: 783) are indicated in Table 10.

Table 9: Bacterial Primer Pairs for Production of Bacterial Bioagent Identifying Amplicons and Corresponding Representative Calibration Sequences

Primer Pair No.	Forward Primer Name	Forward Primer (SEQ ID NO.)	Reverse Primer Name	Reverse Primer (SEQ ID NO.)	Calibration Sequence Model Species	Calibration Sequence (SEQ ID NO.)
361	16S_EC_1090_1111_2_F MOD_F	5	16S_EC_1175_1196_TM0D_R	370	<i>Bacillus anthracis</i>	764
346	16S_EC_713_732_TM0D_F	27	16S_EC_789_809_TM0D_R	369	<i>Bacillus anthracis</i>	765
347	16S_EC_785_806_TM0D_F	30	16S_EC_880_897_TM0D_R	392	<i>Bacillus anthracis</i>	766
348	16S_EC_960_981_TM0D_F	38	16S_EC_1054_1073_TM0D_R	363	<i>Bacillus anthracis</i>	767
349	23S_EC_1826_1843_TM0D_F	49	23S_EC_1906_1924_TM0D_R	405	<i>Bacillus anthracis</i>	768
360	23S_EC_2646_2667_TM0D_F	60	23S_EC_2745_2765_TM0D_R	416	<i>Bacillus anthracis</i>	769
350	CAFC_BA_274_303_TM0D_F	98	CAFC_BA_349_376_TM0D_R	452	<i>Bacillus anthracis</i>	770
351	CYA_BA_1353_1379_TM0D_F	128	CYA_BA_1440_1467_TM0D_R	483	<i>Bacillus anthracis</i>	771
352	INF8_EC_1365_1393_TM0D_F	161	INF8_EC_1439_1467_TM0D_R	516	<i>Bacillus anthracis</i>	772
353	LEF_BA_766_781_TM0D_F	175	LEF_BA_843_872_TM0D_R	531	<i>Bacillus anthracis</i>	773
356	RPLB_EC_650_679_TM0D_F	232	RPLB_EC_739_762_TM0D_R	592	<i>Clostridium botulinum</i>	774
449	RPLB_EC_690_710_F	237	RPLB_EC_737_758_R	589	<i>Clostridium botulinum</i>	775
359	RPOB_EC_1845_1866_TM0D_F	241	RPOB_EC_1909_1929_TM0D_R	597	<i>Yersinia Pestis</i>	776
362	RPOB_EC_3799_3821_TM0D_F	245	RPOB_EC_3862_3888_TM0D_R	603	<i>Burkholderia mallei</i>	777
363	RPOC_EC_2146_2174_TM0D_F	257	RPOC_EC_2227_2245_TM0D_R	621	<i>Burkholderia mallei</i>	778
354	RPOC_EC_2218_2241_TM0D_F	262	RPOC_EC_2313_2337_TM0D_R	625	<i>Bacillus anthracis</i>	779
355	SSFE_BA_115_137_TM0D_F	321	SSFE_BA_197_222_TM0D_R	687	<i>Bacillus anthracis</i>	780
367	TUFB_EC_957_979_TM0D_F	345	TUFB_EC_1034_1058_TM0D_R	701	<i>Burkholderia mallei</i>	781
358	VALS_EC_1105_1124_TM0D_F	350	VALS_EC_1195_1218_TM0D_R	712	<i>Yersinia Pestis</i>	782

Table 10: Primer Pair Gene Coordinate References and Calibration Polynucleotide Sequence Coordinates within the Combination Calibration Polynucleotide

Bacterial Gene and Species	Gene Extraction Coordinates of Genomic or Plasmid Sequence	Reference GenBank GI No. of Genomic (G) or Plasmid (P) Sequence	Primer Pair No.	Coordinates of Calibration Sequence in Combination Calibration Polynucleotide (SEQ ID NO: 783)
16S_E_coli	4033120..4034661	16127994 (G)	346	16..109
16S_E_coli	4033120..4034661	16127994 (G)	347	83..190
16S_E_coli	4033120..4034661	16127994 (G)	348	246..353
16S_E_coli	4033120..4034661	16127994 (G)	361	368..469
23S_E_coli	4166220..4169123	16127994 (G)	349	743..837
23S_E_coli	4166220..4169123	16127994 (G)	360	865..963
rpoB_E_coli	4178923..4182851 (complement strand)	16127994 (G)	359	1591..1672
rpoB_E_coli	4178923..4182851 (complement strand)	16127994 (G)	362	2081..2167
rpoC_E_coli	4182928..4187151	16127994 (G)	354	1810..1926
rpoC_E_coli	4182928..4187151	16127994 (G)	363	2183..2279
infB_E_coli	3313655..3310983 (complement strand)	16127994 (G)	352	1692..1791
tufB_E_coli	4173523..4174707	16127994 (G)	367	2400..2495
rplB_E_coli	3449001..3448180	16127994 (G)	449	1986..2055
rplB_E_coli	3449001..3448180	16127994 (G)	449	1986..2055
valS_E_coli	4481435..4478550 (complement strand)	16127994 (G)	358	1462..1572

capC <i>B. anthracis</i>	56074..55628 (complement strand)	6470151 (P)	350	2517..2616
cys <i>B. anthracis</i>	136826..154286 (complement strand)	4894216 (P)	351	1338..1449
lef <i>B. anthracis</i>	127442..129921	4894216 (P)	353	1121..1234
espE <i>B. anthracis</i>	226496..226783	30253628 (G)	355	1007-1104

[0135] Example 10: Use of a Calibration Polynucleotide for Determining the Quantity of *Bacillus Anthracis* in a Sample Containing a Mixture of Microbes

[0136] The process described in this example is shown in Figure 7. The capC gene is a gene involved in capsule synthesis which resides on the pX02 plasmid of *Bacillus anthracis*. Primer pair number 350 (see Tables 9 and 10) was designed to identify *Bacillus anthracis* via production of a bacterial bioagent identifying amplicon. Known quantities of the combination calibration polynucleotide vector described in Example 3 were added to amplification mixtures containing bacterial bioagent nucleic acid from a mixture of microbes which included the Ames strain of *Bacillus anthracis*. Upon amplification of the bacterial bioagent nucleic acid and the combination calibration polynucleotide vector with primer pair no. 350, bacterial bioagent identifying amplicons and calibration amplicons were obtained and characterized by mass spectrometry. A mass spectrum measured for the amplification reaction is shown in Figure 8). The molecular masses of the bioagent identifying amplicons provided the means for identification of the bioagent from which they were obtained (Ames strain of *Bacillus anthracis*) and the molecular masses of the calibration amplicons provided the means for their identification as well. The relationship between the abundance (peak height) of the calibration amplicon signals and the bacterial bioagent identifying amplicon signals provides the means of calculation of the copies of the pX02 plasmid of the Ames strain of *Bacillus anthracis*. Methods of calculating quantities of molecules based on internal calibration procedures are well known to those of ordinary skill in the art.

[0137] Averaging the results of 10 repetitions of the experiment described above, enabled a calculation that indicated that the quantity of Ames strain of *Bacillus anthracis* present in the sample corresponds to approximately 10 copies of pX02 plasmid.

[0138] Example 11: Drill-down Genotyping of *Campylobacter* Species

[0139] A series of drill-down primers were designed as described in Example 1 with the objective of identification of different strains of *Campylobacter jejuni*. The primers are listed in Table 11 with the designation "CJST_CJ." Housekeeping genes to which the primers hybridize and produce bioagent identifying amplicons include: tkt (transketolase), glyA (serine

hydroxymethyltransferase), gltA (citrate synthase), aspA (aspartate ammonia lyase), glnA (glutamine synthase), pgm (phosphoglycerate mutase), and uncA (ATP synthetase alpha chain).

Table 11: *Campylobacter* Drill-down Primer Pairs

Primer Pair No.	Forward Primer Name	Forward Primer (SEQ ID NO:)	Reverse Primer Name	Reverse Primer (SEQ ID NO:)	Target Gene
1053	CJST CJ 1080 1110 F	102	CJST CJ 1166 1198 R	456	gltA
1064	CJST CJ 1680 1713 F	107	CJST CJ 1795 1822 R	461	glyA
1054	CJST CJ 2060 2090 F	109	CJST CJ 2148 2174 R	463	pgm
1049	CJST CJ 2636 2668 F	113	CJST CJ 2753 2777 R	467	tkt
1048	CJST CJ 360 394 F	119	CJST CJ 442 476 R	472	aspA
1047	CJST CJ 584 616 F	121	CJST CJ 663 692 R	474	glnA

[0140] The primers were used to amplify nucleic acid from 50 food product samples provided by the USDA, 25 of which contained *Campylobacter jejuni* and 25 of which contained *Campylobacter coli*. Primers used in this study were developed primarily for the discrimination of *Campylobacter jejuni* clonal complexes and for distinguishing *Campylobacter jejuni* from *Campylobacter coli*. Finer discrimination between *Campylobacter coli* types is also possible by using specific primers targeted to loci where closely-related *Campylobacter coli* isolates demonstrate polymorphisms between strains. The conclusions of the comparison of base composition analysis with sequence analysis are shown in Tables 12A-C.

Table 12A — Results of Base Composition Analysis of 50 *Campylobacter* Samples with Drill-down MLST Primer Pair Nos: 1048 and 1047

Group	Species	Isolate origin	MLST type or Clonal Complex by Base Composition analysis	MLST Type or Clonal Complex by Sequence analysis	Strain	Base Composition of Bioagent Identifying Amplicon Obtained with Primer Pair No: 1048 (aspA)	Base Composition of Bioagent Identifying Amplicon Obtained with Primer Pair No: 1047 (glnA)
J-1	<i>C. jejuni</i>	Goose	ST 690 /692/707/991	ST 991	RM3673	A30 G25 C16 T46	A47 G21 C16 T25
J-2	<i>C. jejuni</i>	Human	Complex 206/48/353	ST 356, complex 353	RM4192	A30 G25 C16 T46	A48 G21 C17 T23
J-3	<i>C. jejuni</i>	Human	Complex 354/179	ST 436	RM4194	A30 G25 C15 T47	A48 G21 C18 T22
J-4	<i>C. jejuni</i>	Human	Complex 257	ST 257, complex 257	RM4197	A30 G25 C16 T46	A48 G21 C18 T22
J-5	<i>C. jejuni</i>	Human	Complex 52	ST 52, complex 52	RM4277	A30 G25 C16 T46	A48 G21 C17 T23
J-6	<i>C. jejuni</i>	Human	Complex 443	ST 51, complex 443	RM4275	A30 G25 C15 T47	A48 G21 C17 T23
					RM4279	A30 G25 C15 T47	A48 G21 C17 T23
J-7	<i>C. jejuni</i>	Human	Complex 42	ST 604, complex 42	RM1864	A30 G25 C15 T47	A48 G21 C18 T22
J-8	<i>C. jejuni</i>	Human	Complex 42/49/362	ST 362, complex 362	RM3193	A30 G25 C15 T47	A48 G21 C18 T22
J-9	<i>C. jejuni</i>	Human	Complex 45/293	ST 147, Complex 45	RM3203	A30 G25 C15 T47	A47 G21 C18 T23
	<i>C. jejuni</i>	Human	Consistent	ST 828	RM4183	A31 G27 C20 T39	A48 G21 C16 T24

C-1	C. coli	Poultry	with 74 closely related sequence types (none belong to a clonal complex)	ST 832	RM1169	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1056	RM1857	A31 G27 C20 T39	A48 G21 C16 T24
				ST 889	RM1166	A31 G27 C20 T39	A48 G21 C16 T24
				ST 829	RM1182	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1050	RM1518	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1051	RM1521	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1053	RM1523	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1055	RM1527	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1017	RM1529	A31 G27 C20 T39	A48 G21 C16 T24
				ST 960	RM1840	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1063	RM2219	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1066	RM2241	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1067	RM2243	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1068	RM2439	A31 G27 C20 T39	A48 G21 C16 T24
		Swine		ST 1016	RM3230	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1069	RM3231	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1061	RM1904	A31 G27 C20 T39	A48 G21 C16 T24
				Unknown	ST 825	RM1534	A31 G27 C20 T39
		ST 901			RM1505	A31 G27 C20 T39	A48 G21 C16 T24
		C-2		C. coli	Hunan	ST 895	RM1532
C-3	C. coli	Poultry	Consistent with 63 closely related sequence types (none belong to a clonal complex)	ST 1064	RM2223	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1082	RM1178	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1054	RM1525	A31 G27 C20 T39	A48 G21 C16 T24
				ST 1049	RM1517	A31 G27 C20 T39	A48 G21 C16 T24
		Marmoset		ST 891	RM1531	A31 G27 C20 T39	A48 G21 C16 T24

Table 12B – Results of Base Composition Analysis of 50 *Campylobacter* Samples with Drill-down MLST Primer Pair Nos: 1053 and 1064

Group	Species	Isolate origin	MLST type or Clonal Complex by Base Composition analysis	MLST Type or Clonal Complex by Sequence analysis	Strain	Base Composition of Biogent Identifying Amplicon Obtained with Primer Pair No: 1053 (gta)	Base Composition of Biogent Identifying Amplicon Obtained with Primer Pair No: 1064 (gta)
J-1	<i>C. jejuni</i>	Goose	ST 630 /632/707/991	ST 991	RM3673	A24 G25 C23 T47	A40 G29 C29 T45
J-2	<i>C. jejuni</i>	Hunan	Complex 205/48/353	ST 356, complex 353	RM1192	A24 G25 C23 T47	A40 G29 C29 T45
J-3	<i>C. jejuni</i>	Hunan	Complex 354/179	ST 436	RM1194	A24 G25 C23 T47	A40 G29 C29 T45
J-4	<i>C. jejuni</i>	Hunan	Complex 257	ST 257, complex 257	RM4197	A24 G25 C23 T47	A40 G29 C29 T45
J-5	<i>C. jejuni</i>	Hunan	Complex 52	ST 52, complex 52	RM4277	A24 G25 C23 T47	A39 G30 C26 T46
J-6	<i>C. jejuni</i>	Hunan	Complex 443	ST 51, complex 443	RM4275	A24 G25 C23 T47	A39 G30 C28 T46
					RM4279	A24 G25 C23 T47	A39 G30 C28 T46
J-7	<i>C. jejuni</i>	Hunan	Complex 42	ST 604, complex 42	RM1864	A24 G25 C23 T47	A39 G30 C26 T46

J-8	<i>C. jejuni</i>	Human	Complex 42/49/362	ST 362, complex 362	RM3193	A24 G25 C23 T47	A39 G31 C28 T46
J-9	<i>C. jejuni</i>	Human	Complex 45/293	ST 147, Complex 45	RM3203	A24 G25 C23 T47	A39 G31 C28 T46
	<i>C. jejuni</i>	Human		ST 828	RM4183	A23 G24 C26 T46	A39 G30 C27 T47
				ST 832	RM1169	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1056	RM1857	A23 G24 C26 T46	A39 G30 C27 T47
				ST 889	RM1166	A23 G24 C26 T46	A39 G30 C27 T47
				ST 829	RM1182	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1050	RM1518	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1051	RM1521	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1053	RM1523	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1055	RM1527	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1017	RM1529	A23 G24 C26 T46	A39 G30 C27 T47
				ST 860	RM1840	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1063	RM2219	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1066	RM2241	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1067	RM2243	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1068	RM2439	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1016	RM3230	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1069	RM3231	A23 G24 C26 T46	NO DATA
				ST 1061	RM1904	A23 G24 C26 T46	A39 G30 C27 T47
				ST 825	RM1534	A23 G24 C26 T46	A39 G30 C27 T47
				ST 901	RM1505	A23 G24 C26 T46	A39 G30 C27 T47
C-2	<i>C. coli</i>	Human	ST 895	ST 895	RM1532	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1064	RM2223	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1082	RM1178	A23 G24 C26 T46	A39 G30 C27 T47
				ST 1054	RM1525	A23 G24 C25 T47	A39 G30 C27 T47
				ST 1049	RM1517	A23 G24 C26 T46	A39 G30 C27 T47
				ST 891	RM1531	A23 G24 C26 T46	A39 G30 C27 T47
C-1	<i>C. coli</i>	Human	Consistent with 74 closely related sequence types (none belong to a clonal complex)				
		Poultry					
		Swine					
		Unknown					
C-3	<i>C. coli</i>	Human	Consistent with 63 closely related sequence types (none belong to a clonal complex)				
		Poultry					
		Marmoset					

Table 12C – Results of Base Composition Analysis of 50 *Campylobacter* Samples with Drill-down MLST Primer Pair Nos: 1054 and 1049

Group	Species	Isolate origin	MLST type or Clonal Complex by Base Composition analysis	MLST Type or Clonal Complex by Sequence analysis	Strain	Base Composition of Biosystem Identifying Amplicon Obtained with Primer Pair No: 1054 (gcm)	Base Composition of Biosystem Identifying Amplicon Obtained with Primer Pair No: 1049 (tkt)
J-1	<i>C. jejuni</i>	Goose	ST 690 /692/707/991	ST 991	RM3673	A26 G33 C18 T38	A41 G28 C35 T38
J-2	<i>C. jejuni</i>	Human	Complex 206/48/353	ST 356, complex 353	RM4192	A26 G33 C19 T37	A41 G28 C36 T37
J-3	<i>C. jejuni</i>	Human	Complex 354/179	ST 436	RM4194	A27 G32 C19 T37	A42 G28 C36 T36
J-4	<i>C. jejuni</i>	Human	Complex 257	ST 257, complex 257	RM4197	A27 G32 C19 T37	A41 G29 C35 T37
J-5	<i>C. jejuni</i>	Human	Complex 52	ST 52, complex 52	RM4277	A26 G33 C18 T38	A41 G28 C35 T37

J-6	C. jejuni	Human	Complex 443	ST 51, complex 443	RM4275	A27 G31 C19 T38	A41 G28 C36 T37	
					RM4279	A27 G31 C19 T38	A41 G28 C36 T37	
J-7	C. jejuni	Human	Complex 42	ST 604, complex 42	RM1864	A27 G32 C19 T37	A42 G28 C35 T37	
J-8	C. jejuni	Human	Complex 42/49/362	ST 362, complex 362	RM3193	A26 G33 C19 T37	A42 G28 C35 T37	
J-9	C. jejuni	Human	Complex 45/283	ST 147, Complex 45	RM3203	A28 G31 C19 T37	A43 G28 C36 T35	
	C. jejuni	Human	Consistent with 74 closely related sequence types (none belong to a clonal complex)	ST 828	RM4183	A27 G30 C19 T39	A46 G28 C32 T36	
C-1	C. coli			ST 832	RM1169	A27 G30 C19 T39	A46 G28 C32 T36	
				ST 1056	RM1857	A27 G30 C19 T39	A46 G28 C32 T36	
		ST 889		RM1166	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 829		RM1182	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 1050		RM1518	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 1051		RM1521	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 1053		RM1523	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 1055		RM1527	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 1017		RM1529	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 860		RM1840	A27 G30 C19 T39	A46 G28 C32 T36		
		ST 1063	RM2219	A27 G30 C19 T39	A46 G28 C32 T36			
		ST 1066	RM2241	A27 G30 C19 T39	A46 G28 C32 T36			
		ST 1067	RM2243	A27 G30 C19 T39	A46 G28 C32 T36			
		ST 1068	RM2439	A27 G30 C19 T39	A46 G28 C32 T36			
				Swine	ST 1016	RM3230	A27 G30 C19 T39	A46 G28 C32 T36
					ST 1069	RM3231	A27 G30 C19 T39	A46 G28 C32 T36
					ST 1061	RM1904	A27 G30 C19 T39	A46 G28 C32 T36
				Unknown	ST 825	RM1534	A27 G30 C19 T39	A46 G28 C32 T36
		ST 901	RM1505		A27 G30 C19 T39	A46 G28 C32 T36		
C-2	C. coli	Human	ST 895	ST 895	RM1532	A27 G30 C19 T39	A45 G29 C32 T36	
C-3	C. coli	Poultry	Consistent with 63 closely related sequence types (none belong to a clonal complex)	ST 1064	RM2223	A27 G30 C19 T39	A45 G29 C32 T36	
				ST 1082	RM1178	A27 G30 C19 T39	A45 G29 C32 T36	
				ST 1054	RM1525	A27 G30 C19 T39	A45 G29 C32 T36	
				ST 1049	RM1517	A27 G30 C19 T39	A45 G29 C32 T36	
		Marmoset		ST 891	RM1531	A27 G30 C19 T39	A45 G29 C32 T36	

[0141] The base composition analysis method was successful in identification of 12 different strain groups. *Campylobacter jejuni* and *Campylobacter coli* are generally differentiated by all loci. Ten clearly differentiated *Campylobacter jejuni* isolates and 2 major *Campylobacter coli* groups were identified even though the primers were designed for strain typing of

Campylobacter jejuni. One isolate (RM4183) which was designated as *Campylobacter jejuni* was found to group with *Campylobacter coli* and also appears to actually be *Campylobacter coli* by full MLST sequencing.

[0142] Example 12: Identification of *Acinetobacter baumannii* Using Broad Range Survey and Division-Wide Primers in Epidemiological Surveillance

[0143] To test the capability of the broad range survey and division-wide primer sets of Table 4 in identification of *Acinetobacter* species, 183 clinical samples were obtained from individuals participating in, or in contact with individuals participating in Operation Iraqi Freedom (including US service personnel, US civilian patients at the Walter Reed Army Institute of Research (WRAIR), medical staff, Iraqi civilians and enemy prisoners). In addition, 34 environmental samples were obtained from hospitals in Iraq, Kuwait, Germany, the United States and the USNS Comfort, a hospital ship.

[0144] Upon amplification of nucleic acid obtained from the clinical samples, primer pairs 346-349, 360, 361, 354, 362 and 363 (Table 4) all produced bacterial bioagent amplicons which identified *Acinetobacter baumannii* in 215 of 217 samples. The organism *Klebsiella pneumoniae* was identified in the remaining two samples. In addition, 14 different strain types (containing single nucleotide polymorphisms relative to a reference strain of *Acinetobacter baumannii*) were identified and assigned arbitrary numbers from 1 to 14. Strain type 1 was found in 134 of the sample isolates and strains 3 and 7 were found in 46 and 9 of the isolates respectively.

[0145] The epidemiology of strain type 7 of *Acinetobacter baumannii* was investigated. Strain 7 was found in 4 patients and 5 environmental samples (from field hospitals in Iraq and Kuwait). The index patient infected with strain 7 was a pre-war patient who had a traumatic amputation in March of 2003 and was treated at a Kuwaiti hospital. The patient was subsequently transferred to a hospital in Germany and then to WRAIR. Two other patients from Kuwait infected with strain 7 were found to be non-infectious and were not further monitored. The fourth patient was diagnosed with a strain 7 infection in September of 2003 at WRAIR. Since the fourth patient was not related involved in Operation Iraqi Freedom, it was inferred that the fourth patient was the subject of a nosocomial infection acquired at WRAIR as a result of the spread of strain 7 from the index patient.

[0146] The epidemiology of strain type 3 of *Acinetobacter baumannii* was also investigated. Strain type 3 was found in 46 samples, all of which were from patients (US service members, Iraqi civilians and enemy prisoners) who were treated on the USNS Comfort hospital ship and subsequently returned to Iraq or Kuwait. The occurrence of strain type 3 in a single locale may provide evidence that at least some of the infections at that locale were a result of a nosocomial infections.

[0147] This example thus illustrates an embodiment of the present invention wherein the methods of analysis of bacterial bioagent identifying amplicons provide the means for epidemiological surveillance.

[0148] Example 13: Selection and Use of MLST *Acinetobacter baumannii* Drill-down Primers

[0149] To combine the power of high-throughput mass spectrometric analysis of bioagent identifying amplicons with the sub-species characteristic resolving power provided by multi-locus sequence typing (MLST) such as the MLST methods of the MLST Databases at the Max-Planck Institute for Infectious Biology (web.mpiib-berlin.mpg.de/mlst/dbs/Mcatarrhalis/documents/primersCatarrhalis.html), an additional 21 primer pairs were selected based on analysis of housekeeping genes of the genus *Acinetobacter*. Genes to which the drill-down MLST analogue primers hybridize for production of bacterial bioagent identifying amplicons include anthranilate synthase component I (trpE), adenylate kinase (adk), adenine glycosylase (mutY), fumarate hydratase (fumC), and pyrophosphate phospho-hydratase (ppa). These 21 primer pairs are indicated with reference to sequence listings in Table 13. Primer pair numbers 1151-1154 hybridize to and amplify segments of trpE. Primer pair numbers 1155-1157 hybridize to and amplify segments of adk. Primer pair numbers 1158-1164 hybridize to and amplify segments of mutY. Primer pair numbers 1165-1170 hybridize to and amplify segments of fumC. Primer pair number 1171 hybridizes to and amplifies a segment of ppa. The primer names given in Table 13 indicates the coordinates to which the primers hybridize to a reference sequence which comprises a concatenation of the genes TrpE, efp (elongation factor p), adk, mutT, fumC, and ppa. For example, the forward primer of primer pair 1151 is named AB_MLST-11-OIF007_62_91_F because it hybridizes to the *Acinetobacter* MLST primer reference sequence of strain type 11 in sample 007 of Operation Iraqi Freedom (OIF) at positions 62 to 91.

**Table 13: MLST Drill-Down Primers for Identification of Sub-species characteristics
(Strain Type) of Members of the Bacterial Genus *Acinetobacter***

Primer Pair No.	Forward Primer Name	Forward Primer (SEQ ID NO:)	Reverse Primer Name	Reverse Primer (SEQ ID NO:)
1151	AB_MLST-11-OIF007 62 91 F	83	AB_MLST-11-OIF007 169 203 R	426
1152	AB_MLST-11-OIF007 185 214 F	76	AB_MLST-11-OIF007 291 324 R	432
1153	AB_MLST-11-OIF007 260 289 F	79	AB_MLST-11-OIF007 364 393 R	434
1154	AB_MLST-11-OIF007 206 239 F	78	AB_MLST-11-OIF007 318 344 R	433
1155	AB_MLST-11-OIF007 522 552 F	80	AB_MLST-11-OIF007 587 610 R	435
1156	AB_MLST-11-OIF007 547 571 F	81	AB_MLST-11-OIF007 656 686 R	436
1157	AB_MLST-11-OIF007 601 627 F	82	AB_MLST-11-OIF007 710 736 R	437
1158	AB_MLST-11- OIF007 1202 1225 F	65	AB_MLST-11-OIF007 1266 1296 R	420
1159	AB_MLST-11- OIF007 1202 1225 F	65	AB_MLST-11-OIF007 1299 1316 R	421
1160	AB_MLST-11- OIF007 1234 1264 F	66	AB_MLST-11-OIF007 1335 1362 R	422
1161	AB_MLST-11- OIF007 1327 1356 F	67	AB_MLST-11-OIF007 1422 1448 R	423
1162	AB_MLST-11- OIF007 1345 1369 F	68	AB_MLST-11-OIF007 1470 1494 R	424
1163	AB_MLST-11- OIF007 1351 1375 F	69	AB_MLST-11-OIF007 1470 1494 R	424
1164	AB_MLST-11- OIF007 1387 1412 F	70	AB_MLST-11-OIF007 1470 1494 R	424
1165	AB_MLST-11- OIF007 1542 1569 F	71	AB_MLST-11-OIF007 1656 1680 R	425
1166	AB_MLST-11- OIF007 1556 1593 F	72	AB_MLST-11-OIF007 1656 1680 R	425
1167	AB_MLST-11- OIF007 1611 1638 F	73	AB_MLST-11-OIF007 1731 1757 R	427
1168	AB_MLST-11- OIF007 1726 1752 F	74	AB_MLST-11-OIF007 1790 1821 R	428
1169	AB_MLST-11- OIF007 1792 1826 F	75	AB_MLST-11-OIF007 1876 1909 R	429
1170	AB_MLST-11- OIF007 1792 1826 F	75	AB_MLST-11-OIF007 1895 1927 R	430
1171	AB_MLST-11-	77	AB_MLST-11-OIF007 2097 2118 R	431

	OIP007 1976 2002 F			
--	--------------------	--	--	--

[0150] Analysis of bioagent identifying amplicons obtained using the primers of Table 13 for over 200 samples from Operation Iraqi Freedom resulted in the identification of 50 distinct strain type clusters. The largest cluster, designated strain type 11 (ST11) includes 42 sample isolates, all of which were obtained from US service personnel and Iraqi civilians treated at the 28th Combat Support Hospital in Baghdad. Several of these individuals were also treated on the hospital ship USNS Comfort. These observations are indicative of significant epidemiological correlation/linkage.

[0151] All of the sample isolates were tested against a broad panel of antibiotics to characterize their antibiotic resistance profiles. As an example of a representative result from antibiotic susceptibility testing, ST11 was found to consist of four different clusters of isolates, each with a varying degree of sensitivity/resistance to the various antibiotics tested which included penicillins, extended spectrum penicillins, cephalosporins, carbapenem, protein synthesis inhibitors, nucleic acid synthesis inhibitors, anti-metabolites, and anti-cell membrane antibiotics. Thus, the genotyping power of bacterial bioagent identifying amplicons, particularly drill-down bacterial bioagent identifying amplicons, has the potential to increase the understanding of the transmission of infections in combat casualties, to identify the source of infection in the environment, to track hospital transmission of nosocomial infections, and to rapidly characterize drug-resistance profiles which enable development of effective infection control measures on a time-scale previously not achievable.

[0152] Various modifications of the invention, in addition to those described herein, will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. Each reference (including, but not limited to, journal articles, U.S. and non-U.S. patents, patent application publications, international patent application publications, gene bank accession numbers, internet web sites, and the like) cited in the present application is incorporated herein by reference in its entirety.

WHAT IS CLAIMED IS:

1. An oligonucleotide primer selected from the group consisting of: an oligonucleotide primer 16 to 35 nucleobases in length comprising 80% to 100% sequence identity with SEQ ID NO: 26, an oligonucleotide primer 20 to 27 nucleobases in length comprising at least a 20 nucleobase portion of SEQ ID NO: 388, an oligonucleotide primer 22 to 35 nucleobases in length comprising SEQ ID NO: 29, an oligonucleotide primer 18 to 35 nucleobases in length comprising SEQ ID NO: 391, an oligonucleotide primer 22 to 26 nucleobases in length comprising SEQ ID NO: 37, an oligonucleotide primer 20 to 30 nucleobases in length comprising SEQ ID NO: 362, an oligonucleotide primer 13 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 48, an oligonucleotide primer 19 to 35 nucleobases in length comprising SEQ ID NO: 404, an oligonucleotide primer 21 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 160, an oligonucleotide primer 21 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 515, an oligonucleotide primer 17 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 261, an oligonucleotide primer 18 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 624, an oligonucleotide primer 21 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 231, an oligonucleotide primer 17 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 591; an oligonucleotide primer 14 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 349, an oligonucleotide primer 17 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 711, an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 240, an oligonucleotide primer 15 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 596, an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 58, an oligonucleotide primer 21 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 414, an oligonucleotide primer 16 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 6, an oligonucleotide primer 16 to 35 nucleobases in length comprising at least a 16 nucleobase portion of SEQ ID NO: 369, an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 246, an oligonucleotide primer 19 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 602, an oligonucleotide primer 21 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 256, an oligonucleotide primer 14 to 35 nucleobases in length

comprising 70% to 100% sequence identity with SEQ ID NO: 620, an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 344, an oligonucleotide primer 18 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 700, an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 235, an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 587;

wherein said primer comprises a non-templated T residue on the 5'-end, or at least one non-template tag.

2. A composition comprising one or more of the oligonucleotide primers of claim 1.
3. A composition comprising two or more of the oligonucleotide primers of claim 1.
4. The composition of claim 3 wherein either or both of said oligonucleotide primers comprises at least one modified nucleobase.
5. The composition of claim 3 wherein either or both of said oligonucleotide primers comprises a non-templated T residue on the 5'-end.
6. The composition of claim 3 wherein either or both of said oligonucleotide primers comprises at least one non-template tag.
7. The composition of claim 3 wherein either or both of said oligonucleotide primers comprises at least one molecular mass modifying tag.
8. An oligonucleotide primer selected from the group consisting of: an oligonucleotide primer 16 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 322, and an oligonucleotide primer 19 to 35 nucleobases in length comprising 70% to 100% sequence identity with SEQ ID NO: 686.
9. A composition comprising one or both of the oligonucleotide primers of claim 8.
10. The composition of claim 9 wherein either or both of said oligonucleotide primers comprises at least one modified nucleobase.

11. The composition of claim 9 wherein either or both of said oligonucleotide primers comprises a non-templated T residue on the 5'-end.
12. The composition of claim 9 wherein either or both of said oligonucleotide primers comprises at least one non-template tag.
13. The composition of claim 9 wherein either or both of said oligonucleotide primers comprises at least one molecular mass modifying tag.
14. A kit comprising the composition of claim 3 or claim 9.
15. The kit of claim 14 further comprising at least one calibration polynucleotide.
16. The kit of claim 14 further comprising at least one ion exchange resin linked to magnetic beads.
17. A method for identification of an unknown bacterium comprising:
 - amplifying nucleic acid from said bacterium using the composition of claim 3 or claim 9 to obtain an amplification product;
 - determining the molecular mass of said amplification product;
 - optionally determining the base composition of said amplification product from said molecular mass; and
 - comparing said molecular mass or base composition of said amplification product with a plurality of molecular masses or base compositions of known bacterial bioagent identifying amplicons, wherein a match between said molecular mass or base composition of said amplification product and the molecular mass or base composition of a member of said plurality of molecular masses or base compositions identifies said unknown bacterium.
18. The method of claim 17 wherein said molecular mass is determined by mass spectrometry.
19. A method of determining the presence or absence of a bacterium of a particular clade, genus, species, or sub-species in a sample comprising:

amplifying nucleic acid from said sample using the composition of claim 3 or claim 9 to obtain an amplification product;

determining the molecular mass of said amplification product;

optionally determining the base composition of said amplification product from said molecular mass; and

comparing said molecular mass or base composition of said amplification product with the known molecular masses or base compositions of one or more known clade, genus, species, or sub-species bioagent identifying amplicons, wherein a match between said molecular mass or base composition of said amplification product and the molecular mass or base composition of one or more known clade, genus, species, or sub-species bioagent identifying amplicons indicates the presence of said clade, genus, species, or sub-species in said sample.

20. The method of claim 19 wherein said molecular mass is determined by mass spectrometry.

21. A method for determination of the quantity of an unknown bacterium in a sample comprising:

contacting said sample with the composition of claim 3 or claim 9 and a known quantity of a calibration polynucleotide comprising a calibration sequence;

concurrently amplifying nucleic acid from said bacterium in said sample with the composition of claim 3 or claim 9 and amplifying nucleic acid from said calibration polynucleotide in said sample with the composition of claim 3 or claim 9 to obtain a first amplification product comprising a bacterial bioagent identifying amplicon and a second amplification product comprising a calibration amplicon;

determining the molecular mass and abundance for said bacterial bioagent identifying amplicon and said calibration amplicon; and

distinguishing said bacterial bioagent identifying amplicon from said calibration amplicon based on molecular mass, wherein comparison of bacterial bioagent identifying amplicon abundance and calibration amplicon abundance indicates the quantity of bacterium in said sample.

22. The method of claim 21 further comprising determining the base composition of said bacterial bioagent identifying amplicon.

Figure 1

1/8

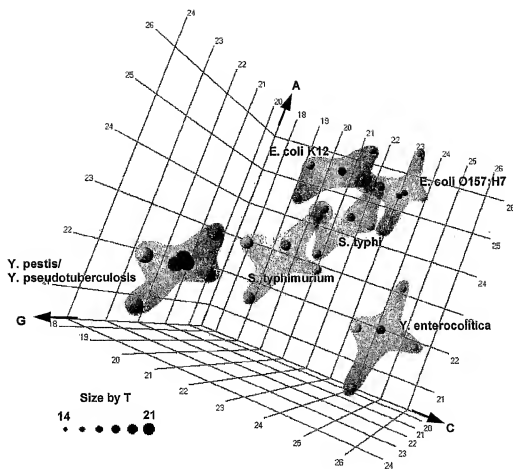
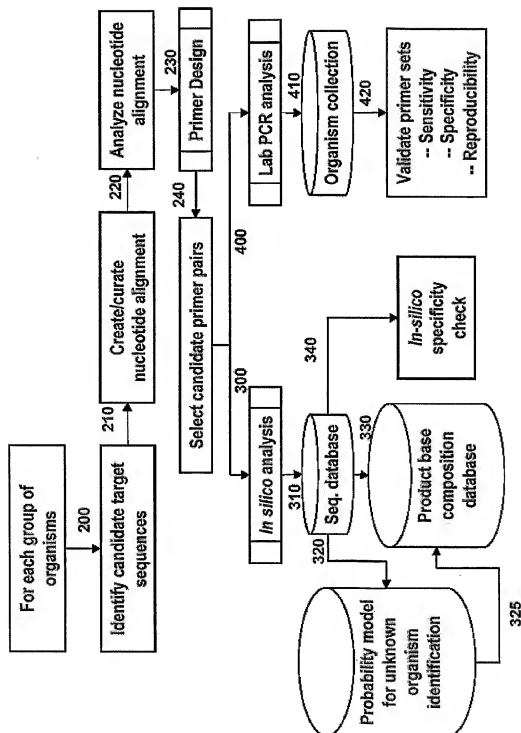


Figure 2



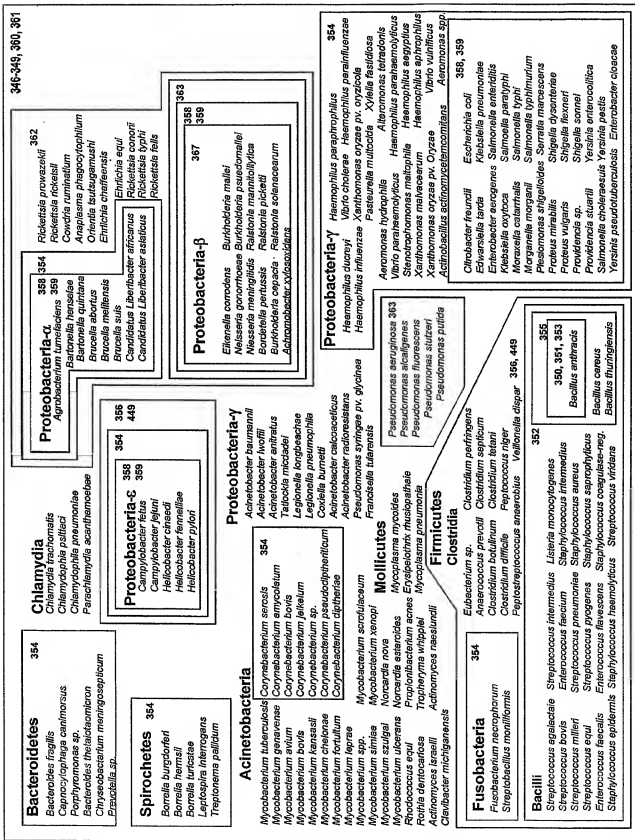


Figure 4

Base Composition Signatures from primer pair 14 (16S rRNA)

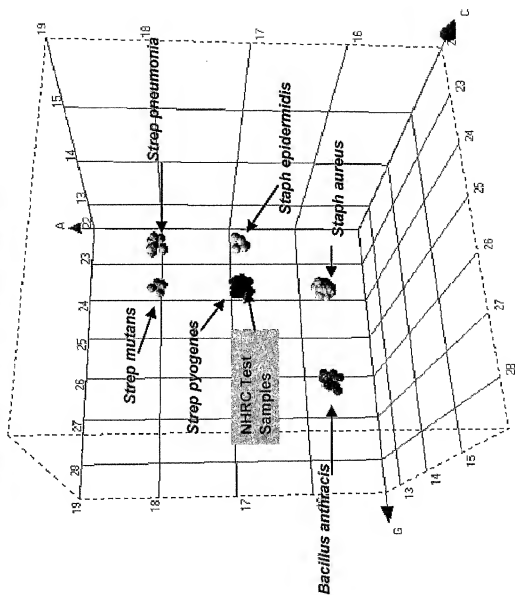


Figure 5

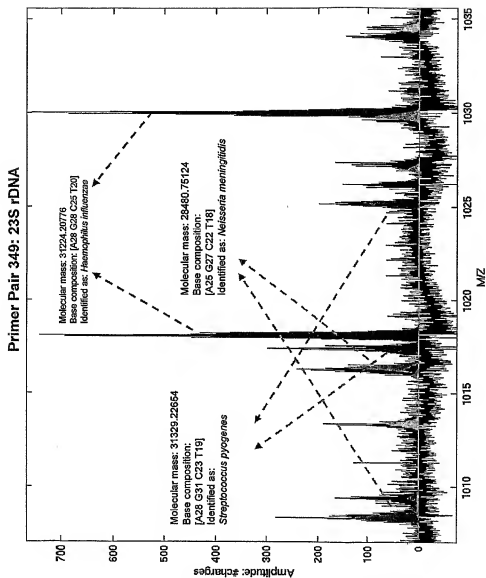


Figure 6

Primer 356: rplB

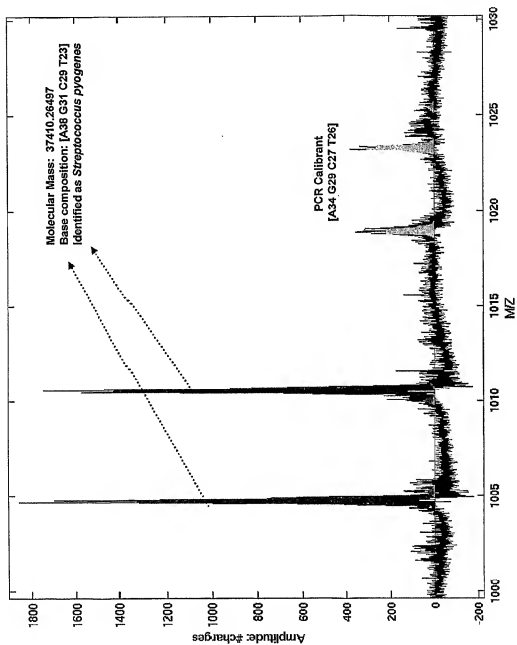


Figure 7

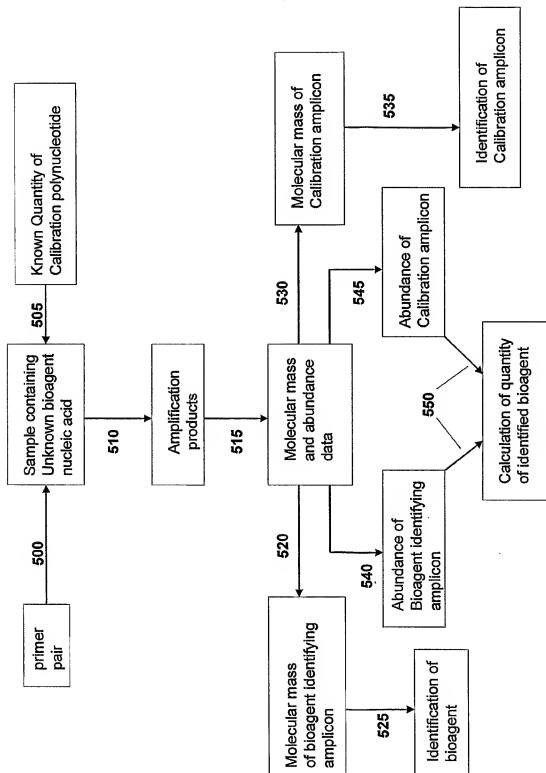
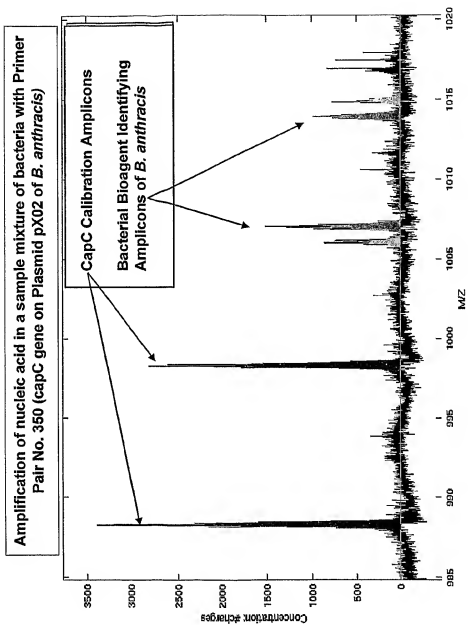


Figure 8



SEQUENCE LISTING

<110> Isis Pharmaceuticals, Inc.
 Sampath, Rangarajan
 Hall, Thomas A.
 Ecker, David J.
 Eshoo, Mark. W.
 Massire, Christian
 Science Applications International Corporation
 Larson, Brons M.
 Leighton, Terrance

<120> COMPOSITIONS FOR USE IN IDENTIFICATION OF BACTERIA

<130> IBIS0074-500WO (DIBIS-0057WO1)

<150> 60/545,425
 <151> 2004-02-18

<150> 60/559,754
 <151> 2004-04-05

<150> 60/632,862
 <151> 2004-12-03

<150> 60/639,068
 <151> 2004-12-22

<150> 60/648,188
 <151> 2005-01-28

<160> 785

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 1
 gtgagatggtt gggtaagtc ccgtaacgag 30

<210> 2
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 2
 atgttgggtt aagtcgcgc 19

<210> 3
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Primer

<400> 3
atgttgggtt aagtcccgca acgag 25

<210> 4
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
ttaagtcccg caacgagcgc aa 22

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
tttaagtccc gcaacgagcgc caa 23

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
ttaagtcccg caacgatcgc aa 22

<210> 7
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
tagtcccgca acgagcgc 18

<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8

caacgagcgc aaccctt 17

<210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 9
 caagtcacga tggeccotta 19

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 10
 gctacacacg tgctacaatg 20

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
 cggattggag tctgcaactc g 21

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 12
 aagtcggaat cgcctagtaac cg 22

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 13
 tacgggtgaat acgttcccg g 21

<210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 14
 gccttgtaca cacctccggt c 21

 <210> 15
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 15
 ettgtacaca ccgcccgtc 19

 <210> 16
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 16
 ttgtacacac cgcccgctat ac 22

 <210> 17

 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 17
 tgaacgctgg tggcatgctt aacac 25

 <210> 18
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 18
 cactggaact gagacacgg 19

 <210> 19
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 19

gtggcatgcc taatacatgc aagtcg 26

<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
tgagtgatga aggccttagg gttgtaaa 28

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
taacacatgc aagtcgaacg 20

<210> 22
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
ccagcagccg cggttaatac 19

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
cggaattact gggcgtaaag 20

<210> 24
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gtgtagcggg gaaatgcg 18

<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer

 <400> 25
 gagagtttga tcttggtca gaacgaa 27

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 26
 agaacacoga tggcgaaggc 20

 <210> 27
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 27
 tagaacacog atggcgaagg c 21

 <210> 28
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 28
 gggagcaaac aggattagat ac 22

 <210> 29
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 29
 ggattagaga ccctggtagt cc 22

 <210> 30
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 30
 tggattagag accctggtag tcc 23

<210> 31
<211> 26
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 31
ggattagata ccctggtagt ccacgc 26

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
tagataccct ggtagtccac gc 22

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 33
gataccctgg tagtccacac cg 22

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 34
agagtttgat catggctcag 20

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 35
accacgccgt aaacgatga 19

<210> 36
<211> 18
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 36

aagcgggtgga gcatgtgg

18

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 37

ttcgatgcaa cggaagaac ct

22

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 38

tttcgatgca acggaagaa cct

23

<210> 39

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 39

acggaagaa ccttacc

17

<210> 40

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 40

acggaagaa ccttacc

17

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 41

gcgaagaacc ttaccaggtc 20

<210> 42
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
cgaagaacct tacc 14

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 43
tgcgcggaag atgtaacggg 20

<210> 44
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 44
tgcatacaaa cagtcggagc ct 22

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
aaactagata acagtagaca tcac 24

<210> 46
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 46
taccocaaac cgacacagg 19

<210> 47
<211> 19

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 47
 ccgttaacttc gggagaagg 19

<210> 48
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 48
 ctgacacctg cccggtgc 18

<210> 49
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 49
 tctgacacct gcccggtgc 19

<210> 50
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 50
 gacgcctgcc cgggtgc 16

<210> 51
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 51
 acctgcccag tgctggaag 19

<210> 52
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 52
gggaactgaa acatctaagt a 21

<210> 53
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 53
ggtggatgcc ttggc 15

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 54
aaggtactcc ggggataaca ggc 23

<210> 55
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 55
tagaacgtcg cgagacagtt cg 22

<210> 56
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 56
gacagttcgg tccctatc 18

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 57
ctgtccctag tacgagagga ccgg 24

<210> 58
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 58
 tctgtcccta gtacgagagg accgg

25

<210> 59
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 59
 ctgttcttag tacgagagga cc

22

<210> 60
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 60
 tctgttctta gtacgagagg acc

23

<210> 61
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 61
 ctagtacgag aggaccgg

18

<210> 62
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 62
 tagtacgaga ggaccgg

17

<210> 63
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220> .
 <223> Primer

 <400> 63
 ggggagtgaag agagatcctg aaaccg 26

 <210> 64
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 64
 cgagaggggaa acaaccocaga cc 22

 <210> 65
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 65
 tcgtgccgcg aatttgcata aagc 24

 <210> 66
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 66
 ttgtagcaca gcaaggcaaa tttcctgaaa c 31

 <210> 67
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 67
 taggtttacg tcagtatggc gtgattatgg 30

 <210> 68
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 68
 tcgtgattat ggatggcaac gtgaa 25

<210> 69
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 69
ttatggatgg caacgtgaaa cgcgt 25

<210> 70
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 70
tctttgccat tgaagatgac ttaagc 26

<210> 71
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 71
tactagcggc aagcttaaac aagattgc 28

<210> 72
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 72
ttgccaatga tattcgttgg ttagcaag 28

<210> 73
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 73
tcggcgaaat ccgtattcct gaaaatga 28

<210> 74
<211> 27
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 74

taccactatt aatgtoctg gtgcttc

27

<210> 75

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 75

ttataactta ctgcaactta ttcagttgct tgggtg

35

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 76

tattgtttca aatgtacaag gtgaagtgcg

30

<210> 77

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 77

tgggttatgta ccaaatactt tgtctgaaga tgg

33

<210> 78

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 78

tgaagtgcgt gatgatatcg atgcacttga tgta

34

<210> 79

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 79

tggaacgtta tcaggtgcc caaaaattcg	30
<210> 80	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 80	
tcggtttagt aaaagaacgt attgctcaac c	31
<210> 81	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 81	
tcaacctgac tgcgtgaatg gttgt	25
<210> 82	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 82	
tcaagcagaa gctttggaag aagaagg	27
<210> 83	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 83	
tgagattgct gaacatttaa tgctgattga	30
<210> 84	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 84	
ttgcttaaag ttggttttat tggttggcg	29
<210> 85	
<211> 34	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Primer

<400> 85

tcagtttttaa tgtctcgtat gatcgaatca aaag 34

<210> 86

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 86

gcacaacctg cggctcgcg 18

<210> 87

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 87

tctagtaata ataggaccct cagc 24

<210> 88

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 88

tatggctcta ctcaa 15

<210> 89

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 89

tgagtcactt gaagttgata caaatcctct 30

<210> 90

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 90
 gaatagcaat taatccaaat 20

 <210> 91
 <211> 24
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 91
 toagttoogt tatgcgaatt goat 24

 <210> 92
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 92
 tggaaactatt gcaactgcta atg 23

 <210> 93
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 93
 tcactottac atataaggaa ggcgcgc 27

 <210> 94
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 94
 tcaggatgga aataaccacc aattcactac 30

 <210> 95
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 95
 gttatttagc actogttttt aatcagcc 28

 <210> 96
 <211> 20

<212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 96
 actcgttttt aatcagcccg 20

<210> 97
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 97
 gattattggt atcctgttat gccatttgag 30

<210> 98
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 98
 tgattattgt tatcctgtta tgccatttga g 31

<210> 99
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 99
 ttattgttat cctgttatgc c 21

<210> 100
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 100
 gttatcctgt tatgccattt g 21

<210> 101
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 101
 ccgtggtatt ggagttattg 20

 <210> 102
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 102
 ttgagggtat gcacogtctt ttgattctt t 31

 <210> 103
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 103
 agttataaac acggtcttcc tatggttat cc 32

 <210> 104
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 104
 tggcttatcc aaatttagat cgtggtttta c 31

 <210> 105
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 105
 ttatcgtttg tggagctagt gcttatgc 28

 <210> 106
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 106
 tgctcgagtg attgactttg ctaaatttag aga 33

<210> 107
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 107
 tgattttgct aaatttagag aaattgcgga tgaa 34

 <210> 108
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 108
 tcccaattaa ttctgccatt ttccagga t 31

 <210> 109
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 109
 tcccggaatt aatatcaatg aaaattgtgg a 31

 <210> 110
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 110
 tgcggatcgt ttggtggtg tagatgaaaa 30

 <210> 111

 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 111
 tcgtttggtg gtggtagatg aaaaagg 27

 <210> 112
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 112

tagatgaaaa gggcgaagtg gctaatgg 28

<210> 113

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 113

tgccctagaag atcttaaaaa tttccgcaaa ctt 33

<210> 114

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 114

tccccaggac accctgaaat ttcaac 26

<210> 115

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 115

tggcatttct tatgaagctt gttctttagc a 31

<210> 116

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 116

tgaagcttgt tctttagcag gacttca 27

<210> 117

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 117 tttgatttta cgccgtcctc caggctcg	27
<210> 118 <211> 34 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 118 tcctgttatc cctgaagtag ttaatcaagt ttgt	34
<210> 119 <211> 35 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 119 tcctgttatc cctgaagtag ttaatcaagt ttgtt	35
<210> 120 <211> 35 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 120 taggcgaaga tatacaaaga gtattagaag ctaga	35
<210> 121 <211> 33 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 121 tccaggacaa atgtatgaaa aatgtccaag aag	33
<210> 122 <211> 34 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 122 tgaaaaatgt ccaagaagca tagcaaaaaa agca	34
<210> 123 <211> 26 <212> DNA	

<213> Artificial Sequence

<220>

<223> Primer

<400> 123

tcttatgccg agaggacaga gtgagt

26

<210> 124

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 124

tgtattaggg gcatacagtc ctcatcc

27

<210> 125

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 125

gaaagagttc ggattggg

18

<210> 126

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 126

acaacgaagt acaatacaag ac

22

<210> 127

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 127

cgaagtacaa tacaagcaa aagaagg

27

<210> 128

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 128 tcgaagtaca atacaagaca aaagaagg	28
<210> 129 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 129 acaatacaag acaaagaag g	21
<210> 130 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 130 caggtttagt accagaacat gcag	24
<210> 131 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 131 ggttagtac cagaacatgc	20
<210> 132 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 132 cggcgtactt caacgacgc ca	22
<210> 133 <211> 32 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 133 ttatcagcta gaccttttag gtaaagctaa gc	32
<210> 134 <211> 32	

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 134
 tccaaggtag actaaactta cttgagctaa tg 32

 <210> 135
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 135
 tcaaaaagcc ctaggtaaag agattccata tc 32

 <210> 136
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 136
 tccgttctta caaatagcaa tagaacttga agc 33

 <210> 137
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 137
 tggagcttga agctatcgct cttaaagatg 30

 <210> 138
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 138
 tgggaacttga agctctcgct cttaaagatg 30

 <210> 139
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 139
 tgggacttga agctatcgct cttaaatgatg 30
 <210> 140
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 140
 tcttctcctc ctatggctat tatgcttgc 29
 <210> 141
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 141
 ggtgaaagaa gttgcctcta aagc 24
 <210> 142
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 142
 atggacaagg ttggcaagga agg 23
 <210> 143
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 143
 aaggaaggcg tgatcaccgt tgaaga 26
 <210> 144
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 144
 tggaagatct gggtcaggc 19

<210> 145
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 145
tctgcccgtg tcgttggtga 20

<210> 146

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 146
tccattgttc gtatggctca agact 25

<210> 147
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 147
tcaggtggct tacacggcgt ag 22

<210> 148
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 148
tctttcttga atgctgggtg acgtatcg 28

<210> 149
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 149
tcaacgaagg taaaaacat ctcaacg 27

<210> 150
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer

 <400> 150
 tgttcgctgt ttcacaaaca acattcca 28

 <210> 151
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 151
 tacttacttg agaatccaca agctgcaa 28

 <210> 152
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 152
 tggcgaacct ggtgaacgaa gc 22

 <210> 153
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 153
 tagttgctca aacagctggg ct 22

 <210> 154
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 154
 tcccggagct tttatgacta aagcagat 28

 <210> 155
 <211> 23
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 155

tcgccgtgga aaaatcctac gct 23

<210> 156
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 156
 ttctcgaccg acccattatt ccctttatc 29

<210> 157
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 157
 tcctgaccga cccattattc cctttatc 28

<210> 158
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 158
 gtctgtaaaa cgagctggaa ga 22

<210> 159
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 159
 tgcgtttacc gcaatgcgtg c 21

<210> 160
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 160
 tgctcgtggt gcacaagtaa cggatatta 29

<210> 161
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 161
 ttgtcgtggg tgcacaagta acggatatta 30

 <210> 162
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 162
 cgtcagggtg aattccgtga agttaa 26

 <210> 163
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 163
 tggtaacaga gccttatagg cgca 24

 <210> 164
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 164
 tgggtccttg gtatgactct gcttc 25

 <210> 165
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 165
 tgttgaggcc tggaccgatt atttac 26

 <210> 166
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 166
 ttatttacct gcactccac aactg 25

<210> 167
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 167
 tccttgaccg ccttccgat ac 22

<210> 168
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 168
 tgaggaccgt gtcgcgtca 20

<210> 169
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 169
 tcagaccatg ctgcgagaga aactt 25

<210> 170
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 170
 tcagtatgta tccaccgtag ccagtc 26

<210> 171
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 171
 tgggtgacat tcatacaatt catcgttc 28

<210> 172
 <211> 17
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 172

tcaagaagaa aaagagc

17

<210> 173

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 173

caagaagaaa aagagcttct aaaaagaata c

31

<210> 174

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 174

agcttttgca tattatatcg agccac

26

<210> 175

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 175

tagcttttgc atattatatc gagccac

27

<210> 176

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 176

cttttgcata ttatatcgag c

21

<210> 177

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 177
 ttacagctt tatgcaccg 19

 <210> 178
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 178
 caacggatgc tggcaag 17

 <210> 179
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 179
 tgtagccgct aagcactacc atcc 24

 <210> 180
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 180
 tggacggcat cagattctc tac 23

 <210> 181
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 181
 tgaagtagaa atgactgaac gtccga 26

 <210> 182
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 182
 taaaacaaac tacggtaaca ttgatcgca 29

 <210> 183

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 183
 tcaggtaactg ctatccaccc tcaa 24

 <210> 184
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 184
 tgtactgcta tccaccctca a 21

 <210> 185
 <211> 11
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 185
 tccaccctca a 11

 <210> 186
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 186
 tcaccagggt caactcaaaa aatattaaca 30

 <210> 187
 <211> 27
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 187
 ttacacatat cgtgagcaat gaactga 27

 <210> 188
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer

<400> 188
ttactccatt attgcttggt tacactttcc 30

<210> 189
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 189
tacacaacaa tggcggtaaa gatgg 25

<210> 190
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 190
tgcgcagctc ttggtatcga gtt 23

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 191
tgctcgaag ctgaatataa ccaagtt 27

<210> 192
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 192
tcaacggtaa cttctatggt acttctg 27

<210> 193
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 193
tcaagccgta cgtattatta ggtgctg 27

<210> 194

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 194
tccgtaacgta ttattaggtg ctggtca

27

<210> 195
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 195
tcgtaacgtat tattaggtgc tggtoact

28

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 196
tggttggtgt ttctggcgct taa

23

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 197
tggtgctttc tggcgcttaa acga

24

<210> 198
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 198
tctaactgatt ttggtaatct tgcagcacag

30

<210> 199
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 199
 tgcaagtggt acttcaacat gggg 24
 <210> 200
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 200
 ttacaggaag ttaggtggt aatctaaaag g 31
 <210> 201
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 201
 cagaatcaag ttcccagggg 20
 <210> 202
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 202
 agaatcaagt tcccaggggt tac 23
 <210> 203
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 203
 aatctgctat ttggtcagg 19
 <210> 204
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 204
 gaaggatata cggttgatgt c 21
 <210> 205

<211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 205
 tcctgaaaaa tggagcacgg 20

<210> 206
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 206
 tggagcacgg cttctgac 19

<210> 207
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 207
 ggctcagcca tttagttacc gctat 25

<210> 208
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 208
 tcagcgcgta cagtggtga t 21

<210> 209
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 209
 tggtgactcg gcatgttatg aagc 24

<210> 210
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 210
 ttataccgga aacttccga aaggag 26

 <210> 211
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 211

 tgacatccgg ctacggtat tatggt 26

 <210> 212
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 212
 tccggctcac gttattatgg tac 23

 <210> 213
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 213
 tgcaaaggag gtactcagac cat 23

 <210> 214
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 214
 tgacatgctt gtcggttcag gc 22

 <210> 215
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 215

tgggtacatgt gccttcattg atgctg 26
 <210> 216
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 216
 tggcacggcc atctccgtg 19
 <210> 217
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 217
 tgcgggtagg gagcttgagc 20
 <210> 218
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 218
 tcctagagga atggctgccg cg 22
 <210> 219
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 219
 taccocaggg aaagtgcac aga 23
 <210> 220
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 220
 taaaccccat cgggagcaag accgaata 28
 <210> 221
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 221

gaggaaagtc catgctcgc

19

<210> 222

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 222

taaggatagt gcaacagaga tataccgcc

29

<210> 223

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 223

gaggaaagtc cgggctc

17

<210> 224

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 224

tctaaatggt cgtgcagttg cgtg

24

<210> 225

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 225

tggtaaagagc gcaccggtaa gttggtaaca

30

<210> 226

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 226	
taagagcgca ccggttaagtt gg	22
<210> 227	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 227	
tgcataccgg taagttggca aca	23
<210> 228	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 228	
tccaccaaga gcaagatcaa ataggc	26
<210> 229	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 229	
gaggaaagtc catgctcac	19
<210> 230	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 230	
tccgcgagtg tgaactgggt	19
<210> 231	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 231	
gacctacagt aagaggttct gtaatgaacc	30
<210> 232	
<211> 31	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Primer

<400> 232

tgacctacag taagagggttc tgtaatgaac c 31

<210> 233

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 233

tgtaatgaac octaatgacc atccacacgg 30

<210> 234

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 234

taatgaaccc taatgaccat ccacacggtg 30

<210> 235

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 235

catccacacg gtggtggtga agg 23

<210> 236

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 236

tcatccacac ggtggtggtg aagg 24

<210> 237

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 237
 tccacacggt ggtggtgaag g 21

 <210> 238
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 238
 gaccacctcg gcaaccgt 18

 <210> 239
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 239
 tcagctgtcg cagttcatgg acc 23

 <210> 240
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 240
 tatcgctcag gcgaactcca ac 22

 <210> 241
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 241
 ttatcgctca ggcgaactcc aac 23

 <210> 242
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 242
 tcgttcctgg aacacgatga cgc 23

 <210> 243
 <211> 29

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 243
 tcaacaacct cttggaggta aagctcagt 29

 <210> 244
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 244
 cttggaggta agtctcattt tgggtgggca 29

 <210> 245
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 245
 tgggcagcgt ttggcgaaa tgga 24

 <210> 246
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 246
 gggcagcgtt tcggcgaaat gga 23

 <210> 247
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 247
 cagcgtttcg gcgaaatgga 20

 <210> 248
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 248
 caaaacttat taggtaagcg tgttgact 28
 <210> 249
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 249
 cgtgttgact attcggggcg ttcag 25
 <210> 250
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 250
 taagaagccg gaaaccatca actaccg 27
 <210> 251
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 251
 acccagtgct gctgaacogt gc 22
 <210> 252
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 252
 cgcgacttc gacggtgacc 20
 <210> 253
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 253
 tcgccgactt cgacggtgac c 21

<210> 254
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 254
 tggcccgaaa gaagctgagc g 21

<210> 255
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 255
 tcaggagtcg ttcaactcga totacatgat g 31

<210> 256
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 256
 caggagtcgt tcaactcgat ctacatgat 29

<210> 257
 <211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 257
 tcaggagtcg ttcaactcga totacatgat 30

<210> 258
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 258
 tgattcgggt gcccgtygt 19

<210> 259
 <211> 19
 <212> DNA
 <213> Artificial Sequence


```

<220>
<223> Primer

<400> 259
tgattctggt gccggtggt
19

<210> 260
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 260
cttgctggta tgcgtggtct gatg
24

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 261
ctggcaggta tgcgtggtct gatg
24

<210> 262
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 262
tctggcaggat atgcgtggctc tgatg
25

<210> 263
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 263
tggtatgcgt ggtctgatgg c
21

<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 264
tgctcgtaag ggtctggcgg atac
24

```

<210> 265
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 265
 cgtcgtgtaa ttaaccgtaa caaccg

26

<210> 266
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 266
 cgtcgggtga ttaaccgtaa caaccg

26

<210> 267
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 267
 tattggacaa cggtcgtcgc gg

22

<210> 268
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 268
 tctggataac ggtcgtcgcg g

21

<210> 269
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 269
 caaaggtaa g caagcagtt tccgtca

27

<210> 270
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 270
 caaaggtaag caaggtcgtt tccgtca 27

 <210> 271
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 271
 aaccttaatt ggaagaaac ccaagaagt 29

 <210> 272
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 272
 taaccttaat tggaagaaa cccaagaagt 30

 <210> 273
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 273
 caataccgca acagcggtg cttggg 26

 <210> 274
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 274
 tcaataccgc aacagcggtg gcttggg 27

 <210> 275
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 275

gctgggtgaaa ataaccaga tgtcgtcttc 30

<210> 276
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 276
 tgcgtggtgaa aataaccag atgtcgtctt c 31

<210> 277
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 277
 cgcaaaaaaa tccagctatt agc 23

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 278
 tcgcaaaaaa atccagctat tagc 24

<210> 279
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 279
 cgagttagc taaaaaata gtttatgaca 30

<210> 280
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 280
 tcgagttagc ctaaaaaat agtttatgac a 31

<210> 281
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 281
 cctatattaa tcgtttacag aaactggct 29
 <210> 282
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 282
 tcctatatatta atcgtttacaa gaaactggct 30
 <210> 283
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 283
 ctggcgtaaaa ctttggcaac ggt 23
 <210> 284
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 284
 tctggctaaa actttggcaa cggt 24
 <210> 285
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 285
 atgattacaa ttcaagaag tcgtcacgc 29
 <210> 286
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 286
 tatgattaca attcaagaag gtcgtcacgc 30
 <210> 287
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 287
 taacgggttat catggcccag atggg 25
 <210> 288
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 288
 ttaacgggta tcatggccca gatggg 26
 <210> 289
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 289
 agcaggtggt gaaatgggc acatgatt 28
 <210> 290
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 290
 tagcaggtgg tgaaatgggc cacatgatt 29
 <210> 291
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 291
 cagagaccgt ttatcctat cagc 24
 <210> 292

<211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 292
 tcagagaccg ttttattccta tcagc

 <210> 293
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 293
 ttctaaacac caggtcaccc agaag

 <210> 294
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 294
 ttctaaaaca ccaggctacc cagaag

 <210> 295
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 295
 atggccatgg cagaagctca

 <210> 296
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 296
 tatggccatg gcagaagctc a

 <210> 297
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

25

25

26

20

21

<400> 297
 cttgtacttg tggctcacac ggctgtttgg 30

 <210> 298
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 298
 tcttgtactt gtggctcaca cggctgtttg g 31

 <210> 299
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 299
 accatgacag aaggcatttt gaca 24

 <210> 300
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 300
 taccatgaca gaaggcattt tgaca 25

 <210> 301
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 301
 gatgactttt tagctaattg tcaggoagc 29

 <210> 302
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 302
 tgatgacttt ttagctaattg gtcaggcagc 30

 <210> 303

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 303
tagctaattgg tcaggcagcc 20

<210> 304
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 304
gtcaaaagtg cacgtttact ggc 23

<210> 305
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 305
tgtcaaaagtg gcacgtttac tggc 24

<210> 306
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 306
agcgtaaagg tgaacctt 18

<210> 307
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 307
tagcgtaaag gtgaacctt 19

<210> 308
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer

 <400> 308
 gcttcaggaa tcaatgatgg agcag 25

 <210> 309
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 309
 tgcttcaggga atcaatgatg gagcag 26

 <210> 310
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 310
 ggggattcag ccatcaaagc agctattgac 30

 <210> 311
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 311
 tggggattca gccatcaaag cagctattga c 31

 <210> 312
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 312
 tcagccatca aagcagctat tg 22

 <210> 313
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>

 <223> Primer

 <400> 313

ccttacttcg aactatgaat cttttggaag 30
 <210> 314
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 314
 tccttacttc gaactatgaa tcttttgga g 31
 <210> 315
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 315
 ggggattgat atcacgata agaagaa 27
 <210> 316
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 316
 tggggattga tatcacgat aagaagaa 28
 <210> 317
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 317
 tgcgaatca aaactaaggg aatggc 26
 <210> 318
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 318
 ttgcgaatc aaaactaagg gaatggc 27
 <210> 319
 <211> 29
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 319

gggcaacagc agcggattgc gattgogcg

29

<210> 320

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 320

tgggcaacag cagcggattg cgattgogcg

30

<210> 321

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 321

tcaagcaaac gcacaatcag aagc

24

<210> 322

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 322

caagcaaacg cacaatcaga agc

23

<210> 323

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 323

aaagcacaat cagaagc

17

<210> 324

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 324
 tgcaaatca gaagctaaga aagcgcaagc t 31
 <210> 325
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 325
 tgcaagcttc tgggtgctagc att 23
 <210> 326
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 326
 tgcttctggg gctagcatt 19
 <210> 327
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 327
 tgggtgctagc att 13
 <210> 328
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 328
 tgctagttat ggtacagagt ttgcgac 27
 <210> 329
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 329
 tgggtacagag ttgcgac 18
 <210> 330
 <211> 15

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 330
 tacagagttt gcgac 15

<210> 331
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 331
 tcgattaggg agcaacgaaa gcgg 24

<210> 332
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 332
 tcgacctttg gcaggaacta gac 23

<210> 333
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 333
 tcaaatgtac aaggtgaagt gcgtga 26

<210> 334
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 334
 tggatggcat ggtgaaatgg atatgtc 27

<210> 335
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 335
 atgtcgattg caatccgtac ttgtg 25

 <210> 336
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 336
 gtgcatgcgg atacagagca gag 23

 <210> 337
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 337
 tgcaagcgcg accacatacg 20

 <210> 338
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 338
 gcactatgca cactagatt gtcctgg 27

 <210> 339
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 339
 ttgactgccc aggtcacgct g 21

 <210> 340
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 340
 tagactgccc aggacacgct g 21

<210> 341
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 341
 tgcacgcccga ctatgttaag aacatgat 28

 <210> 342
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 342
 tgatcactgg tgctgctcag atgga 25

 <210> 343
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 343
 aagacgacct gcacgggc 18

 <210> 344
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 344
 ccacacgccc ttcttcaaca act 23

 <210> 345
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 345
 tccacacgcc gttcttcaac aact 24

 <210> 346
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 346
 aactaccgtc ctcagttcta cttec 25

 <210> 347
 <211> 25
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 347
 aactaccgtc cgcagttcta cttec 25

 <210> 348
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 348
 ccacagttct acttcogtac tactgacg 28

 <210> 349
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 349
 cgtggcggcg tggttatcga 20

 <210> 350
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 350
 tcgtggcggc gtggttatcg a 21

 <210> 351
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 351
 tatgctgacc gaccagtggc acgt 24

<210> 352
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 352
 cgacgcgctg cgcttcac 18

<210> 353
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 353
 cttctgcaac aagctgtgga acgc 24

<210> 354
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 354
 accgagcaag gagaccagc 19

<210> 355
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 355
 tcttgctctt tcgtgagttc agtaaatg 28

<210> 356
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 356
 tcgatctggc ttcattgctgt ttcagt 26

<210> 357
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 357
 ttactcaccc gtcgcgcgt 20

 <210> 358
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 358
 tgttactcac cgtctgcc ct 22

 <210> 359

 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 359
 ttactcaccc gtcgcgc 17

 <210> 360
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 360
 acaaccatgc accacctgtc 20

 <210> 361
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 361
 taagcattac tcaccgcgc gc 22

 <210> 362
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 362

acgagctgac gacagccatg	20
<210> 363	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 363	
tacgagctga cgacagccat g	21
<210> 364	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 364	
acgacacgag ctgacgac	18
<210> 365	
<211> 12	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 365	
acacgagctg ac	12
<210> 366	
<211> 15	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 366	
tccccacctt cctcc	15
<210> 367	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 367	
gacgtcatcc ccaccttcct cc	22
<210> 368	
<211> 21	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Primer

<400> 368

gacgtcatcc ccaccttctc c

21

<210> 369

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 369

tgacgtcatc cccaccttcc tc

22

<210> 370

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 370

ttgacgtcat cccaccttc etc

23

<210> 371

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 371

ttgacgtcat cccaccttc etc

23

<210> 372

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 372

tgacgtcatg gccaccttcc

20

<210> 373

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 373
 tgacgtcatg cccaccttcc 20

 <210> 374
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 374
 tgacgtcatc cccaccttcc 20

 <210> 375
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 375
 attgtagcac gtgtgtagcc c 21

 <210> 376
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 376
 cgagttgcag actgcgatcc g 21

 <210> 377
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 377
 cgagttgcag actgcgatcc g 21

 <210> 378
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 378
 gacgggcggt gtgtacaag 19

 <210> 379
 <211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 379

accttggtac gacttcaccc ca

22

<210> 380

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 380

ccttggtacg acttcacccc

20

<210> 381

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 381

cacggctacc ttggtacgac

20

<210> 382

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 382

aaggaggtga tccagcc

17

<210> 383

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 383

actgctgcct ccgtag

17

<210> 384

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer
 <400> 384
 cggtgctgg cacgaagta g 21
 <210> 385
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 385
 cttaacgcc agtaattccg 20
 <210> 386
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 386
 cgcatttcac cgctacac 18
 <210> 387
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 387
 gtatotaate ctgtttgctc cc 22
 <210> 388
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 388
 cgtggactac cagggtatct a 21
 <210> 389
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 389
 tcgtggacta ccagggtatc ta 22

<210> 390
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 390
cgtactcccc aggcg

15

<210> 391
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 391
ggccgtactc cccaggcg

18

<210> 392
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 392
tggccgtact ccccaggcg

19

<210> 393
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 393
gcgaccgtac tccccagg

18

<210> 394

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 394
gccttgcgac cgtactccc

19

<210> 395
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 395
cccccgctcaa ttcttttgag t 21

<210> 396
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 396
ggtaagggttc ttgcggttg 19

<210> 397
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 397
tcgcagggtt acagaacgct ctctta 26

<210> 398
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 398
tcggactcgc ttctgctaag 20

<210> 399
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 399
gtgcgcctt tctaactt 18

<210> 400
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 400
tggctgcttc taagccaac 19

<210> 401
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 401
 ggggtttccc attcgg 16

<210> 402
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 402
 ccttctcccg aagttacg 18

<210> 403
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 403
 caccgggcag gcgtc 15

<210> 404
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 404
 gaccgttata gttacggc 19

<210> 405
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 405
 tgaccgttat agttacggc 20

<210> 406
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 406
 tcgctacctt aggacggt 18

 <210> 407
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 407
 ccgacaagga atttcgctac c 21

 <210> 408
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 408
 ttcgctcgcc gctac 15

 <210> 409
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 409
 agccgacatc gaggtgccaa ac 22

 <210> 410
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 410
 ccggtcctct cgtacta 17

 <210> 411
 <211> 20
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 411

agtcacatccc ggtcctctcg 20

<210> 412
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 412
 ttagatgctt tcagcactta tc 22

<210> 413
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 413
 acttagatgc ttccagcggg 20

<210> 414
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 414
 tgcttagatg ctttcagc 18

<210> 415
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 415
 ttctgtgctta gatgctttca g 21

<210> 416
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 416
 ttctgtgctt agatgctttc ag 22

<210> 417
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 417
 gtttcattgct tagatgcttt cagc 24

 <210> 418
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 418
 acaaaaaggca cgccatcaac c 21

 <210> 419
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 419
 acaaaaaggta cgccgtcaac c 21

 <210> 420
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 420
 taatgccggg tagtgcaatc catttttcta g 31

 <210> 421
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 421
 tgcacctgcy gtcgagcy 18

 <210> 422
 <211> 28
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 422
 tgccatccat aatcacgccca tactgacg 28
 <210> 423
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 423
 tgccagtttc cacatttcac gtctgtg 27
 <210> 424
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 424
 tcgcttgagt gtagtcatga ttgcg 25
 <210> 425
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 425
 tgagtcgggt tcactttacc tggca 25
 <210> 426
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 426
 ttgtacattt gaaacaatat gcatgacatg tgaat 35
 <210> 427
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 427
 taccggaagc accagcgaca ttaatat 27
 <210> 428
 <211> 32

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 428
tgcaactgaa tagattgcag taagtataa gc 32

<210> 429
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 429
tgaattatgc aagaagtgat caattttcto acga 34

<210> 430
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 430
tgccgtaact aacataagag aattatgcaa gaa 33

<210> 431
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 431
tgacggcatc gataccaccg tc 22

<210> 432
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 432
tcacagggtc tacttcocatc ataatttcca ttgc 34

<210> 433
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 433
 tccgccaataa actccccctt tcacagg 27

 <210> 434
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 434
 ttgcaatoga catatccatt tcaccatgcc 30

 <210> 435
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 435
 ttctgcttga ggaatagtc gtgg 24

 <210> 436
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 436
 taogttctac gattttctca tcaggtacat c 31

 <210> 437
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 437
 tacaacgtga taaacacgac cagaago 27

 <210> 438
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 438
 tccatattgt tgcataaaac ctgttggc 28

 <210> 439

<211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 439
 tcgagatgtcg aaaaaaacgt tggcaaaata c 31

<210> 440
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 440
 acggcacgag gtagtcgc 18

<210> 441
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 441
 taaccatttc gcgtaagatt caa 23

<210> 442
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 442
 tcacgtgcta atgttactgc tggatctg 28

<210> 443
 <211> 14
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Primer

<400> 443
 tgttactgct ggat 14

<210> 444
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer
 <400> 444
 ttactttctaa cccaactc 17
 <210> 445
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 445
 tgcgggctgg ttcaacaaga g 21
 <210> 446
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 446
 tgatgcgggc tggttcaac 19
 <210> 447
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 447
 tcctgtttta tagcgccaa gagtaag 27
 <210> 448
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 448
 tcaaggttct cacggtttac cttaggag 28
 <210> 449
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 449
 tgaatcttga aacaccatac gtaacg 26
 <210> 450

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 450
 tgaatcttga aacaccat-ac g 21

<210> 451
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 451
 gtaacccttg tctttgaatt gtatttgc 28

<210> 452
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 452
 tgtaaccctt gcttttga at tgtatttgc 29

<210> 453
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 453
 ggtaaccctt gcttttgaat 20

<210> 454
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 454
 tggtaaccct tgtctttg 18

<210> 455
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 455
tcccttattt ttctttctac taccttcgga taat 34

<210> 456
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 456
tccctcatg tttaaatgat caggataaaa agc 33

<210> 457
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 457
tcgggtttaag ctctacatga tcgtaaggat a 31

<210> 458
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 458
tttgctcatg atctgcatga agcataaa 28

<210> 459
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 459
tgcaatgtgt gctatgtcag caaaaagat 29

<210> 460
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 460
tgagcgtgtg gaaaaggact tggatg 26

<210> 461
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 461
 tatgtgtagt tgagcttact acatgagc 28

<210> 462
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 462
 tgggtctttac ttgcttttgc taaactttcc a 31

<210> 463
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 463
 tcgatccgca tcaccatcaa aagcaaa 27

<210> 464
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 464
 tcacactgg attgtaattt acctgtttot tt 32

<210> 465
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 465
 tctctttcaa agcaccattg ctcatatag t 31

<210> 466
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 466
 tgaattctttt caaagcacca ttgctcatta tagt 34

 <210> 467
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 467

 ttgctgccat agcaaagcct acagc 25

 <210> 468
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 468
 tgtgtctttt ttgctgccat agcaaagc 28

 <210> 469
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 469
 tgcttcaaaa cgcattttta cattttcggt aaag 34

 <210> 470
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 470
 tcctccttgt gcttcaaac gcattttta 29

 <210> 471
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 471
 tcaaagaacc cgcacctaat tcctcattta 30

<210> 472
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 472
 tcaactgggtt caaaaacatt aagttgtaat tgtcc 35

 <210> 473
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 473
 tacaactgggt tcaaaaacat taagctgtaa ttgtc 35

 <210> 474
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 474
 ttcatTTTTCT ggtccaaagt aagcagtatc 30

 <210> 475
 <211> 33
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 475
 tcccgaaacaa tgagttgtat caactatttt tac 33

 <210> 476
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 476
 tgcctaacaa atcccgctctg agttc 25

 <210> 477
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 477
 tgtcatcaag caccctcaaaa tgaact 26
 <210> 478
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 478
 ccacttttaa taagggtttgt agc 23
 <210> 479
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 479
 tgttgaccat gcttcttag 19
 <210> 480
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 480
 cttctacatt tttagccatc ac 22
 <210> 481
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 481
 cggcttcaag acccc 15
 <210> 482
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 482
 tgtaacggc ttcaagaccc 20

<210> 483
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 483
 ttgttaacgg cttcaagacc c 21

 <210> 484
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 484
 accactttta ataaggtttg tagctaac 28

 <210> 485
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 485
 cgcggtcggc tcgttgatga 20

 <210> 486
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 486
 tcacctacag ctttaaagcc agcaaatg 29

 <210> 487
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 487
 tttctgttaa agggtggttt attatcctc cca 33

 <210> 488
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 488

tagccttggc aacatcagca aaact

25

<210> 489

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 489

ttggcgacgg tatacccata gotttata

28

<210> 490

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 490

tgaacatttg cgacgtata cccat

25

<210> 491

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 491

tgtgaacatt tgcgacggta taccoat

27

<210> 492

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 492

tgggggggat cttagcaatc attctaataag c

31

<210> 493

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 493

tcgcgatggta ggtatcttag caatcattct	30
<210> 494	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 494	
caatctgctg acggatctga gc	22
<210> 495	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 495	
ttcaggtcca tcgggttcat gcc	23
<210> 496	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 496	
ccgcggtcga attgcatgcc ttc	23
<210> 497	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 497	
tagccgcggt cgaattgcat	20
<210> 498	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 498	
tcgaaccgaa gttaccctga ccat	24
<210> 499	

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 499
 tgccagctta gtcatacgga cttc 24

 <210> 500
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 500
 tattgoggat caccatgatg atattcttgc 30

 <210> 501
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 501
 tcgttgagat gggtttttacc ttctgttg 27

 <210> 502
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 502
 tttgtgaaac agcgaacatt ttcttggta 29

 <210> 503
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 503
 tcacgcgcac catcaccagt ca 22

 <210> 504
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer

<400> 504
tcttgcaata tctaatagcac tcttacg 27

<210> 505
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 505
aactgcaata tctaatagcac tcttacg 27

<210> 506
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 506
ctttgcgttt ctggaactca accat 25

<210> 507
<211> 22
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 507
tagcccagct gtttgagcaa ct 22

<210> 508
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 508
tcacctaatag tagaataaac tgcacagta gc 32

<210> 509
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 509
tcacctaatag tagaataaac tgcacagta gc 32

<210> 510
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 510
taggattttt ccacggcggc atc 23

<210> 511
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 511
tagccttttc tccggcgtag atct 24

<210> 512
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 512
catgatgggc acaaccgg 18

<210> 513
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 513
tcggcatcac gccgtcgtc 19

<210> 514
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 514
tgetgcttgc gcatggttaa ttgcttcaa 29

<210> 515
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer

 <400> 515
 ttgctgcttt cgcattggtta attgcttcaa 30

 <210> 516
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 516
 aacttcgcct tcggtcatgt t 21

 <210> 517
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 517
 ttgogttgca gattatcttt accaa 25

 <210> 518
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 518
 tgttaagtgt gttgggctg tctttatt 28

 <210> 519
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 519
 tcacggcagc agtgccatcc attg 24

 <210> 520
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 520
 tgacccaaag ctgaaagctt tactg 25

<210> 521
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 521
 ttttc**c**agcc atgcagcgac 20

 <210> 522
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 522
 tcctt**c**tgat gcctgatgga ccaggag 27

 <210> 523
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 523
 tgtca**c**tccc gacacgcca 19

 <210> 524
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 524
 taaac**g**tcg ataccaatgg ttgcgtc 27

 <210> 525
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 525
 tcaaca**a**acac ctcttatttc ccactc 26

 <210> 526
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 526
 gaatatcaat ttgttagc 17

 <210> 527
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 527
 agataaagaa tcacgaatat caatttgtag c 31

 <210> 528
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 528
 aggatagatt tattttottgt tog 23

 <210> 529
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 529
 ttttccaagg atagatttat ttcttggttcg 30

 <210> 530
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 530
 ttcttccaag gatagattta ttcttggttc g 31

 <210> 531
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 531
 ttttgacagc atccgttg 18
 <210> 532
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 532
 cagataaaga atcgctccag 20
 <210> 533
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 533
 tctcatccgc atattaccgc catga 25
 <210> 534
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 534
 tggcaacagc tcaacacctt tgg 23
 <210> 535
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 535
 tgatcctgaa tgtttatatc ttttaacgcct 30
 <210> 536
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 536
 tcccaateta acttccacat accatct 27
 <210> 537
 <211> 27

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 537
 tggatagacg tcatatgaag gtgtgct 27

 <210> 538
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 538
 tattttctgt tactcatgcc ataca 25

 <210> 539
 <211> 11
 <212> DNA

 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 539
 tactcatgcc a 11

 <210> 540
 <211> 11
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 540
 tattttctgt t 11

 <210> 541
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 541
 taaccacccc aagatttato tttttgcc 29

 <210> 542
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 542
tgtgatatgg aggtgtagaa ggtgtta 27

<210> 543
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 543
gagctgcgcc aacgaataaa togtc 25

<210> 544
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 544
tacgtgcgct ttaacttggt tatattcagc 30

<210> 545
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 545
tgccgtaaca tagaagttac cgttgatt 28

<210> 546
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 546
tcggggogtag ttttttagtaa ttaaatcaga agt 33

<210> 547
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 547
tcgtcgtatt tatagtgacc agcaccta 28

<210> 548

<211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 548
 tcaacaccag cgttacctaa agtacctt 28

 <210> 549
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 549
 ttttaagcgcc agaaagcacc aac 23

 <210> 550
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 550
 togtttaagc gccagaaagc accaa 25

 <210> 551
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 551
 taagccagca agagctgtat agttcca 27

 <210> 552
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 552
 tacaggagca gcaggttca ag 22

 <210> 553
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer

<400> 553
tagcagcaaaa agttatcaca cctgcagt 28

<210> 554
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 554
tggttgtagt tcctgtagtt gttgcattaa c 31

<210> 555
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 555
tcctgcagct ctacctgctc catta 25

<210> 556
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 556
ccctgtagta gaagaggtaa ccac 24

<210> 557
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 557
cctgtagtag aagaggtaac 20

<210> 558
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 558
tgattatcag cggaagtag 19

<210> 559
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 559
 ccgtgctcca tttttcag 18

<210> 560
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 560
 toggataagc tgccacaagg 20

<210> 561
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 561
 toggataagc tgccacaagg 20

<210> 562
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 562
 ttccctgac cttogattaa aggatagc 28

<210> 563
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 563
 ggtataacgc atcgagcaa aagattta 28

<210> 564
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 564
 ttccgtataa cgcattgcag ca 22

 <210> 565
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 565
 tcgctcagca ataattcact ataagcga 29

 <210> 566
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 566
 taatgcgata ctggcctgca agtc 24

 <210> 567
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 567
 tgtaaattcc gcaaagactt tggcattag 29

 <210> 568
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 568
 tggctctgagt acctcctttg c 21

 <210> 569
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 569
 tattggaat accggcagca tctc 24

<210> 570
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 570
 ttcaagtgct tgctcaccat tgctc 24

 <210> 571
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 571
 tggctcataa gacgcgcttg taga 24

 <210> 572
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 572
 togtttcacc ctgtcatgcc g 21

 <210> 573
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 573
 tccgataagc cggattctgt gc 22

 <210> 574
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 574
 tgccgataag ccggattctg tgc 23

 <210> 575
 <211> 27
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Primer
 <400> 575
 tctcttacc caccctttca cctttac 27
 <210> 576
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 576
 tgctctgtgc aaccaccgcg 20
 <210> 577
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 577
 tgctctgcgc aacctaccgc 20
 <210> 578
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 578
 gtaagccatg ttttgttcca tc 22
 <210> 579
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 579
 tttaacctgc ctttccacc ttacc 25
 <210> 580
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 580

tgctcttacc tcaccgttcc acccttacc	29
<210> 581	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 581	
ataagccggg ttctgtcg	18
<210> 582	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 582	
tctatagagt ccggacttcc ctctgtga	27
<210> 583	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 583	
tcaagcgatc taccgcatt acaa	24
<210> 584	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 584	
ataagccatg ttctgttcca tc	22
<210> 585	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 585	
tgactttcct ccccttacc agtctcc	27
<210> 586	
<211> 27	
<212> DNA	
<213> Artificial Sequence	

<220>
 <223> Primer

 <400> 586
 ccaagtgctg gtttacccca tggagta 27

 <210> 587
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 587
 gtgctggttt accccatgga gt 22

 <210> 588
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 588
 tgtgtgggtt taccocatgg agt 23

 <210> 589
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 589
 tgtgtgggtt taccocatgg ag 22

 <210> 590
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 590
 tccaagtgtc ggtttaccoc atggag 26

 <210> 591
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 591 tccaagtgtc ggtttacccc atgg	24
<210> 592 <211> 25 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 592 ttccaagtgc tggtttacc catgg	25
<210> 593 <211> 29 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 593 tgttttgtat ccaagtgtc gtttacc	29
<210> 594 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 594 ttcgctctcg gctgggc	18
<210> 595 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 595 tcgtcgcgga ctctgaagcc	20
<210> 596 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 596 gctggattcg cttttgctac g	21
<210> 597	

<211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 597
 tgctggattc gcctttgcta cg 22

 <210> 598
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 598
 ttgacgttgc atgttogaga ccat 24

 <210> 599
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 599
 cgtataagct gcaccataag cttgtaatgc 30

 <210> 600
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 600
 tttcttgaag agtatgagct gctccgtaag 30

 <210> 601
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 601
 cgacttgacg gttaacattt octg 24

 <210> 602
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 602 gtccgacttg acggtcaaca ttctctg	27
<210> 603 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 603 tgtccgactt gacggtcaac atttctg	28
<210> 604 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 604 tgtccgactt gacggttagc atttctg	28
<210> 605 <211> 28 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 605 tgtccgactt gacggtcagc atttctg	28
<210> 606 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 606 tccagcaggt tctgacggaa acg	23
<210> 607 <211> 26 <212> DNA <213> Artificial Sequence	
<220> <223> Primer	
<400> 607 ttaccgagca ggttctgacg gaaacg	26
<210> 608	

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 608
 cgaa cggcca gagtagtcaa cacg 24

 <210> 609
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 609
 cgaa cggcct gagtagtcaa cacg 24

 <210> 610
 <211> 30

 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 610
 tcaa ggcga tctctttcgg taatccacat 30

 <210> 611
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 611
 tcaa ggcga tttcttttgg taaaccacat 30

 <210> 612
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 612
 attcaagagc cattttctttt ggtaaacac 30

 <210> 613
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer

<400> 613
gttcaaatgc ctggataccc a 21

<210> 614
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 614
gagcatcagc gtgcgtgct 19

<210> 615
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 615
tgagcatcag cgtgcgtgct 20

<210> 616
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 616
acgcgggcat gcagagatgc c 21

<210> 617
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 617
ggcgcttgta cttaccgcac 20

<210> 618
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 618
ttggcctatca gaccacgcac ac 22

<210> 619

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 619
ttggccatca ggccacgcat ac

22

<210> 620
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 620
acgccatcag gccacgcat

19

<210> 621
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 621
tacgccatca ggccacgcat

20

<210> 622
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 622
ttacgccatc aggccacgca

20

<210> 623
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 623
cgcaccatgc gtagagatga agtac

25

<210> 624
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 624
cgcaccgtgg gttgagatga agtac

25

<210> 625
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 625
tcgcaccgtg ggttgagatg aagtac

26

<210> 626
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 626
tgctagacct ttacgtgcac cgtg

24

<210> 627
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 627
tactagacga cgggtcaggt aacc

24

<210> 628
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 628
gtttttcgtt gcgtacgatg atgtc

25

<210> 629
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 629

acgttttttcg ttttgaacga taatgct 27

<210> 630
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 630
 gaccccaacc tggccttttg tcgttga 27

<210> 631
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 631
 tgaccccaac ctggcctttt gtcgttga 28

<210> 632
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 632
 aaactatttt ttttagctata ctogaacac 29

<210> 633
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 633
 taaactattt ttttagctat actogaacac 30

<210> 634
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 634
 ggataattgg tcgtaacaag ggatagtgag 30

<210> 635
 <211> 31
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 635

tggataattg gtcgtaacaa gggatagtga g

31

<210> 636

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 636

atatgattat cattgaactg cggccg

26

<210> 637

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 637

tatatgatta tcattgaact gcggccg

27

<210> 638

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 638

gcgtgacgac cttcttgaat tgtaatca

28

<210> 639

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 639

tgcgtagcga ccttcttgaa ttgtaatca

29

<210> 640

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 640
 ttggacctgt aatcagctga atactgg 27

 <210> 641
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 641
 tttggacctg taatcagctg aatactgg 28

 <210> 642
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 642
 attgccaga aatcaaatca tc 22

 <210> 643
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 643
 tattgccag aatcaaatc atc 23

 <210> 644
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 644
 tgtggccgat ttcaccacct gctcct 26

 <210> 645
 <211> 27

 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 645
 ttgtggccga tttcaccacc tgctcct 27

 <210> 646
 <211> 23

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 646
 tctgggtgac ctgggtgtttt aga 23

<210> 647
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 647
 ttctgggtga cctgggtgttt taga 24

<210> 648
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 648
 agctgctaga tgagcttctg ccatggcc 28

<210> 649
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 649
 tagctgctag atgagcttct gccatggcc 29

<210> 650
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 650
 ccataaggtc accgtcacca ttcaaagc 28

<210> 651
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 651
 tccataaggt caccgtcacc attcaaagc 29
 <210> 652
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 652
 ggaatttacc agcgatagac acc 23
 <210> 653
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 653
 tggaatttac cagcgataga cacc 24
 <210> 654
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 654
 tgccactttg acaactcctg ttgctg 26
 <210> 655
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 655
 ttgccacttt gacaactcct gttgctg 27
 <210> 656
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 656
 aatcgacgac catcttggaa agattttctc 29
 <210> 657

<211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 657
 taatcgacga ccatcttgga aagatttctc 30

 <210> 658
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 658
 tcgacgacca tcttggaag atttc 25

 <210> 659
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 659
 ccagcagtta ctgtccctc atctttg 27

 <210> 660
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 660
 tccagcagtt actgtccct catctttg 28

 <210> 661
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 661
 gctgctttga tggctgaatc cccttc 26

 <210> 662
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer

<400> 662
 tggtggtttg atggctgaat ccccttc 27

<210> 663
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 663
 gggctctacac ctgcacttg ataac 25

<210> 664
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 664
 tgggtctaca cctgcacttg cataac 26

<210> 665
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 665
 atccccctgt tctgtgtgcc 19

<210> 666
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 666
 tateccctgc ttctgtgtgc 20

<210> 667
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>
 <223> Primer

<400> 667
 tacottttcc acaacagaat cagc 24

<210> 668
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 668
 ccaacaccttt ccacaacaga atcagc 26

 <210> 669
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 669
 tccaaccttt tcacaacag aatcagc 27

 <210> 670
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 670
 cccatttttt cagcgtgct gaaaatatc 29

 <210> 671
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 671
 tccatttttt tcacgcatgc tgaaaatatc 30

 <210> 672
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 672
 gattggcgat aaagtgatat ttctataaa 29

 <210> 673
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 673
 tgattggcga taaagtgata ttttctaaaa 30

 <210> 674
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 674
 gccaccaga aagactagca ggataa 26

 <210> 675
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 675
 tgcccaccag aaagactagc aggataa 27

 <210> 676
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 676
 octacccaac gttcaccaag ggcag 25

 <210> 677
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 677
 toctacccaa cgttcaccaa gggcag 26

 <210> 678
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 678
 catgacagcc aagacctcac ccacc 25

<210> 679
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 679
 tcatgacagc caagacctca cccacc 26

<210> 680
 <211> 15

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 680
 tgtgctttga atgct 15

<210> 681
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 681
 tcatttgtgc ttggaatgct 20

<210> 682
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 682
 tcataactag catttgtgct ttggaatgct 29

<210> 683
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 683
 ttgcacgtct gtttcagttg caaatc 27

<210> 684
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

 <400> 684
 ttgcacgtct gtttcagttg caaatte 27

 <210> 685
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 685
 tctgtttcag ttgcaaatte 20

 <210> 686
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 686
 tgcacgtctg tttcagttgc aaattc 26

 <210> 687
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 687
 ttgcacgtct gtttcagttg caaatte 27

 <210> 688
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 688
 ttccacagca tgcacgtctg tttcagttgc 30

 <210> 689
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 689

ttgtgattgt ttgcagctg attgtg	26
<210> 690	
<211> 13	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 690	
tgacagctgat tgt	13
<210> 691	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 691	
tgattgtttt gcagctgatt gt	22
<210> 692	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 692	
ttcaaaacct tgctctcgcc aaacaa	26
<210> 693	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 693	
tacatcgttt cgccaagat caatca	26
<210> 694	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Primer	
<400> 694	
tctctttttt acaggctcta cttcatc	27
<210> 695	
<211> 30	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Primer

<400> 695

tatttgggtt tcattccact cagattctgg

30

<210> 696

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 696

tgcgcgagct tttatttggg ttcc

24

<210> 697

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 697

ttcaaaatgc ggaggcgat gtg

23

<210> 698

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 698

tgcccaggta caacctgcat

20

<210> 699

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 699

tccaggcatt accatttcta ctcttctgg

30

<210> 700

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 7 00
 ggcacaccca ttcccttgct cctcg 25
 <210> 7 01
 <211> 2 6
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 7 01
 tggcacaccc attccttgct cctcg 26
 <210> 7 02
 <211> 2 4
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 7 02
 gttgtcacca ggcattacca ttcc 24
 <210> 7 03
 <211> 2 4
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 7 03
 gttgtgcaca ggcataacca ttcc 24
 <210> 7 04
 <211> 2 1
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 7 04
 gccgtccatt tgagcagcac c 21
 <210> 7 05
 <211> 2 1
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 7 05
 gccgtccatt tgagcagcac c 21
 <210> 7 06
 <211> 2 6

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 706
 tatagcacca tccatctgag cggcac 26

 <210> 707
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 707
 tatgtgctca cgagtttgcg gcat 24

 <210> 708
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 708
 tggatgtgct cagagtcctg tggcat 26

 <210> 709
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 709
 gcgctccacg tcttcacg 19

 <210> 710
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 710
 acgaactgga tgtcgccgtt 20

 <210> 711
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

<400> 711
 cggtaacgaac tggatgtgc cgtt 24
 <210> 712
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 712
 toggtaacgaa ctggatgtgc ccgtt 25
 <210> 713
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 713
 ttccgcgcac caggagaagt acatgtt 27
 <210> 714
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 714
 gcgttccaca gcttgttgca gaag 24
 <210> 715
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 715
 tcgcagttca tcagcacgaa ggc 23
 <210> 716
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 716
 tataacgcac atcgtcaggg tga 23
 <210> 717

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 717
 caagcgggttt gctcacaata gtca

24

<210> 718
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 718
 tggcacgagc ctgacctgt

19

<210> 719
 <211> 1542
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Escherichia coli

<400> 719
 aaatgtgaaga gtttgcacat ggcctcagatt gaaogctggc ggcaggccta acacatgcaa 60
 gtcgaacggt aacaggaaga agcttgcttc tttgctgacg agtggcggac gggtagtaa 120
 tgtctgggaa actgcctgat ggaggggat aactactgga aacggtagct aataccgat 180
 aacgtgcga gacaaaagag ggggaccttc gggcctcttg ccactggatg tgcccagatg 240
 gggattagcta gtagggtggg taacggctca cctaggcgac gatccctagc tggctctgaga 300
 ggatgaccag ccacactgga actgagacac ggtccagact cctacgggag gcagcagtg 360
 ggaatatgct acaatgggag caagcctgat gcagccatgc cgcgtgtatg aagaaggcct 420
 tcgggtgtta aagtacttcc agcggggagg aagggagtaa agttaatacc tttgctcatt 480
 gaogttaccc gcagaagaag caccggctaa ctccgtgcca gcagccggg taatacggag 540
 ggtgcaagcg ttaactggaa ttactgggag taaagcgac gcagcgggtt tgttaagta 600
 gatgtgaaat ccccgggctc aacotgggaa ctgoatctga tactggcaag cttgagtctc 660
 gttagggggg gtgaatttcc aggtgttagc gtgaaatcgc tagagatctg gaggaaatac 720
 ggtggcgaa gcggccccct ggacgaagac tgacgctcag gtgcgaaagc ttggggagca 780
 aacaggatta gataccctgg tagtccacgc cgtaaacgat gtgcacttgg aggtttgtgc 840
 cttgaggcgt ggccttcogga gctaaccgct taagtcgacc gctggggagc tacggccgca 900
 aggttaaaac tcaaatgaat tgacgggggc ccgcacaagc ggtggagcat ttggtttaat 960
 tcgatgcaac gcgaagaacc ttactcgttc ttgacatcca cggaaagttt cagagatgag 1020
 aatgtgcctt cgggaacgct gagacaggtg ctgcactgct gtctgcagct cgtgttgtaga 1080
 aatgttggtt taagtccccc aacgagcgca acccttatcc tttgttgcca gcggtcocgg 1140
 cgggaactca aaggagactg ccagtataaa actggagcaa ggtggggatg acgtcaagtc 1200
 atcatggccc ttacgaccag ggtacacac gtgctcaaat ggcgcataca aagagaagcg 1260
 accctgcgag agcaagcgga cctcataaag tgcgtcgtag tccggattgg agtctgcaac 1320
 tcgactccat gaagtcgaaa tcgctagtaa tcgtggatca gaatgccagc gtgaatacgt 1380
 tcccggccct tgtacacacc gccctgcaca ccatggcagc ggttgcaaca agaagtagt 1440
 agcttaacct tcgggagggc gcttaccact ttgtgatcca tgactgggtg gaagtctgta 1500
 caaggttaacc gttaggggac ctgcggttgg atccacctcc ta 1542

<210> 720
 <211> 2904

<212> DNA

<213> Artificial Sequence

<220>

<223> Escherichia coli

<400> 720

```

ggtttaagcga ctaagcgtag acggtggatg cctggcag cagaggcgat gaaggacgtg 60
ctaattctgcg ataagctgcg gtaaggtgat atgaaccgtt ataacccggc atttccgaat 120
ggggaaacccc atgtgtgtttc gacacactat oattaactga atccataggc taatgaggcg 180
aacccggggga actgaacacat ctaagtaccoc ogaggaaaag aaatcaaccg agattccccc 240
agtagcgccgc agcgaacggg gagcagccca gacgtgaat cagtggtgtg gtagtgggaa 300
gogtctggaa aggcgcgcga tacagggtga cagcccgcta caaaaaatg cacaatgctg 360
gagctcgatg agtagggcgg gacacgtggt atcctgtotg aatatggggg gaccatccct 420
caaggctaaa tactcctgac tgacogtaga tgaaccagta cogtgaggga aaggcgaaaa 480
gaaccccgcgc gaggggagtg aaaaaaaccc tgaaccggtg tacgtacaag cagtgggagc 540
acgottaggcg gtgtgactgc gtaacctttg tataatgggt cagcgactta tattctctag 600
caaggttaac ccgaatgggg agccgaaggg aaaccgagtc ttaactgggc gtttaagttgc 660
agggatataga ccogaaaaccc ggtgatctag ccatggcgag gttgaagggt gggtaacact 720
aactggagga ccgaaccgac taatgttgaa aaattagcgg atgactgtgt gctggggggtg 780
aaagggccaat caaacccggga gatagctggt totcccga aaagotatttag gttagcgccct 840
gtgaattcat cctccggggt agagcactgt ttccggcaag gggctatccc gacttaccaa 900
ccogagtgoa actcogaata ccggagaatg ttatcacggg agacacacgg cgggtgtctaa 960
cgctcgttgt gaagagggaa acaaccoga cccgcagcta aggtcccaaa gtcattggta 1020
agtgccagtc gatgtgggaa ggccacagac gacaggtatg tggottgaaa catcatcaca 1080
tttaagaaaa gogtaatagc toactggctg agtggccotg ccgggaagat gtaacggggc 1140
taaacatctc accgaagctg cggcagcgac gcttatcggt tggttggtag gggagcgctg 1200
tgtaatactgc cgaaggtgtg ctgtgaggca tgctggaggt atcagaatgt cgaatgctga 1260
cataagtaaac gataaagcgg gtgaaaagcc ogctgcggcg aagaccaaag gttccctgtcc 1320
aacgttaatc ggggcagggg gagtogaacc ctaaggcgag gccgaagggt gtagtcgatg 1380
ggaaacaggt taatatctct gtaactgtgt ttaactcgaa ggggggacgg agaaggtcat 1440
gttgccggcg cgaaggttgt cccgggtttaa gogttagagg tggttttcca gggaaactcc 1500
gaaaatcaag gctgagcgct gatgacgagg cactacgggt ctgaagcaac aaatgcctct 1560
cttccagtaa aagctcttaa gcatcaggtt acatcaaatc taaccccaaa ccgacacagg 1620
tggtcggtta gagaatacca aggcgcttga gagaactcgg gtaaggaaac taggcaaaa 1680
gggtccgtgaa cticgggaga aggcacgctg atatgtaggt gaggtccctc gggagtggag 1740
ctgaatacag togaagatag cagctggctg caactgttta ttaaaaacac agcaactgtc 1800
aaacacgaaa gtggacgtat acggtgtgac gctgcgccg tgccgggaag ttaattgatg 1860
gggttagcgc aagcgaagct cttgatcgaa gccccggtaa accggcgccg taactataac 1920
gggtcctaagg tagtogaatt ccttgtcggg taagttccga cctgcacgaa tggogtaagt 1980
atggccagcg tbtctccaac cgagactcag tgaattgaa ctcgctgtga agatgcagtg 2040
tacccggcgc aagaagcgaaa gaccccgtag aocotttacta tagottgaca ctgaacattg 2100
agccttgatg tctaggtatg gtgggagcgt ttgaagtgtg gacgcagcgc tgcattggagc 2160
cgactgtgaa ataccacccgt ttaatgtttg atgttctaac gttgacccgt aatccggggt 2220
cgggacagtg tctggtgggt agtttgtaog gggcggtctc ctccataaag gtaacggagg 2280
agcaggaagg ttggctaatc ctggtcggag atcaggaggt tagtgcattg gataagacca 2340
gottgactgc gacgtgagc gcgcgagcag gtgcgaaagc aggtcatagt gatccggtg 2400
ttctgaattg aagggccatc gctcaacgga taaaaggtag tccgggggta accagggtgat 2460
accggccaaag agttccatate gacggcggtg ttggcacct cgaatgctgc tcacatcact 2520
ctggggctga agtaggtccc aagggtatg ctgttogcaa ttttaagtgg taccgagagt 2580
gggtttagaa cgtctgtaga cagttcgctc ootatctgco gttggcgctg gagaactgag 2640
gggggtctgc actagtacga gaggacccga gtaggacgat caotgggtgt gctgtgtcca 2700
tgccaatggc actcccggtt agotaaatcg ggaagagata agtgcgtgaa gcatctaaag 2760
acgaaacttg accccgagat agttctccct gaccccttaa gggctcctgaa ggaacgttga 2820
agacgacgac gttgatagcg cgggtgtgta agcgcagcga tgcgttgtagc taaccggtag 2880
taatgaacgc tgagccttaa cctt

```

<210> 721

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> *Bacillus anthracis*

<400> 721

```

atgtttggat cagatttata tattgcatta gtattaggag ttacaotgag ccttattttt 60
acagaaagaa caggtatttt acctgcaggt ttagtgttac ctgggtattt agcaotcgtt 120
tttaactcagc caggtatttt ttattttatc gtattttaac atatgtaatc 180
gttacgtatg gtgtttcaag attcatgatt ttatatggcc gtagaaaatt tgcggcaacg 240
ctaattacag gtattttgtt aaaactttta ttgtattatt ttatcctgtt taatgcattt 300
gagatttttg aattcctgtg taitggagtt attgttccag gattaattgc aaatacaatt 360
caaagacaag gggtaccatt aacaattgga actacaattt ttgtaagtgg tgcacaattt 420
gcaatcatga atatttatta cttatttt 447

```

<210> 722

<211> 2339

<212> DNA

<213> Artificial Sequence

<220>

<223> *Bacillus anthracis*

<400> 722

```

atgaactagaa ataaaatttat acctaatag tttagtatta tatccttttc agtattacta 60
tttgctatat cctctccaca ggctatagaa gtaaatgcta tgaatgaaca ttacactgag 120
agtgatatta aaagaaacca taaaactgaa aaaaataaaa ctgaaaaaga aaaaatttaa 180
gacagtatta taactcttagt taaaacagaa tttaaccaatg aaactcttaga taaaatacag 240
cagacacaag acttatttaa aaagatacct aaggatgtac ttgaaattta taagtgaatta 300
ggaggagaaa tctattttac agatatagat tttagtagaac ataaaggagtt acaagattta 360
agtgaagaag agaaaaatag tatgaatagt agaggtgaaa aagttccgtt tgcactccgt 420
tttgattttg aaaaagaaag ggaacacact aaattaatta taaatatcaa agattatgca 480
attaactagt aacaaagttaa agaagtatat tatgaattg gaaaggagat tctcttgtat 540
attataagta aggataaact tctagatcca gagtttttaa atttaattaa gagttttaagc 600
gatgatagtg atagtagcga ccttttattt agtcaaaaaa ttaaaagaga ctagaatttg 660
aataataaaa gtatagatat aaattttata aaagaaaatt taactgaatt tccagctatg 720
ttttcttttg cgttttttta ttattttgca cctgaaccata gaacggtatt agagttatat 780
gcccccgaca tgttttgatg tatgaataag ttgaaaaaag ggggatttga gaaaaatagt 840
gaaagtttga agaaagaagg tgtgaaaaaa gataggattg atgtgctgaa aggagaaaaa 900
gcacttaaa cttacggttt agtaccagaa catgcagatg cttttaaaaa aattgctaga 960
gaattaaata cttattttct ttttaggcct gttaataagt tagctacaaa ctttattaaa 1020
agtggtgtgg ctacaaagagg attgaatggt catggaaaaga gttcggatga tggccctgta 1080
ctggtataca taccatttga tcaagattta tctaagaagc atggctcaaca attagctgtc 1140
gagaaaggaa atttagaaaa taaaaaatca attacagago atgaaggtga aatagattga 1200
atccoattaa agttaagcca ttaagaataa gaagagttaa aggaaaaatgg gataattttg 1260
aagggttaaa aagaaattga taatggtaaa aaattatttt ttgttagaat gaaataacag 1320
gtatatgaat ttagaattag cgtatgaaac aacgaagtac atatacaagac aaagaagggt 1380
aaaattactg ttttagggga aaaattcaat tggagaaata tagaagtatg ggtcaaaaaa 1440
gtagaagggg tcttgagacc gttaacagct gactatgatt tatttgact tgcctcaagt 1500
ttaacagaaa taaaaaaaca aataccacaa aaagaatggg ataaagtatg taacacccca 1560
aattcattag aaaaagcaaaa aggtgttact aattttattg ttaaatattg aattagaggt 1620
aaacggattt caactaaggg aactttatca aattggcaaa acaaaaatgtc tgaatcgttg 1680
aatgaacagc tcaaatatag aggatataca gggggggatg tggltatacca tggcacagag 1740
caagataatg aagagtttcc tgaaaaagat aacgaaattt ttataattaa tccagaagggt 1800
gaatttatat taactaaaaa ttggggagatg acaggtagat ttatagaaaa aacactaacg 1860
ggaaaagatt atttatatta ttttaaccgt tttataataa aaatagctcc tggtaataaa 1920
gcttatattg agtggactga tccgattaca aaagccaaaa taatatacct cctcactgca 1980
cgagagttta taaaaaactt atccagtac agaagatctt caaatgtagg cgtttataaa 2040
tgagtgtggc acaaaagaca atttgcaaaa aaagaagagc tgaaaaaaat tgcgagattat 2100
ttgttcagat attcaaatc agcaaaatcat attttttctc agaaaaaaaa gcgtaaaaaa 2160
tcaattattc gtggaattcca agcctataat gaattgaaa atgttctaaa a.tctaaaaa 2220
atagcaccag aatacaaaaa ttattttcaa tattttaaag aaggattac c.aatcaagg 2280

```

caattgtctc taacacatca aaaatctaatt attgaattta aattattgtg taaacaatt 2339

<210> 723

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> *Escherichia coli*

<400> 723

```

atgggttaaaa taattgggat cgaactgggt actaccaact cttgtgtagc gattatggat 60
ggcaccactc ctgcgctgct ggagaacgoc gaaggcgatc gcaaacgccc ttotatcatt 120
gcctataccc aggatgggtg aactctagtt ggtcagccgg ctaaacgtca ggcagtgaac 180
aaccccgcaaa acactctggt tgcgattaaa ccctgattg gtccgctgtt ccaggagtaa 240
gaagtacagc gtgatgttct catcatgcgc ttcaaaatta ttgctgtcga taacggcgac 300
gcactgggtc aagttaaaag ccagaaaaat gcaocgcgcg agatttctgc tgaagtgtct 360
aaaaaaatga agaaaaacgc tgaagattac ctgggtgaac cggttaactg agctgttatt 420
accgtaccgg catactttaa cgtatgctcag cgtcaggcaa ccaagacgca agccgtattc 480
gctgtctcgg aagtaaaacg tatcatcaac gaacgcagcc cagctgcgct ggtcttaccgt 540
ctgggacaaag gcaactggcaa ccgtactatc gcggtttatg acctgggttg ttgtactttc 600
gatatttcta ttatcgaaat cgaacgaagt gacggcgaaa aaaccttcga agttctggca 660
accaacgggtg ataccacact ggggggtgaa gaactcgaca ccgctctgat caactatctg 720
gttgaagaat tcaagaaaga tcagggcatt gaactgcgca acgatccgct ggcgaatcga 780
cgctgaaag aagcggcgaga aaaagcgaaa atcgaaactgt ctccgctgca ccagaccgac 840
gttaactcgc catatcatca tcagacgcgc accggtccga aacacatgaa catcaaaagt 900
actcgtgcga aactggaaag cctggttgaa gatctggtaa accgttccat tgacccgctg 960
aaagtgtcac tgcaggaagc tggcctgttc gtatctgata tcgaacgact gacggctgtt 1020
ggtgtctaga ctggtatgcc aatggttcag aagaaagtgt ctgagtcttt tggtaagag 1080
cccgctaaag acgttaaccc ggacgaagct gtgacaaatc gtgctgtgtt tcaaggctgt 1140
gttctgactg gtgacgtaaa agacgtactg ctgctggagc ttaccctcgt gtctctgggt 1200
atcgaaaaca tggcggtgtg gatgacgacg ctgatcgcaa aaaaacacac tatcccgacc 1260
aagcacagcc aggtgtttct taccgctgaa gacaaaccgt ctgcggtaac catccatgtg 1320
ctgcagggtg aacgttaaac tgcgcgtgat acaaaactct tgggtcagtt caactatgat 1380
ggtatcaacc cggcaccgcg cggcatgccg cagatcgaa gttaccttga tatcgatgtc 1440
gacggtatcc tgcacgtttc cgcgaaagat aaaaacagc gtaaaagcaa gaagatcacc 1500
atcaaggctt ctctgtgtct gaacgaagat gaaatccaga aatggtagc cgacgcagaa 1560
gctaacgcgc aagctgaccc taagtgtgaa gagctggtac agactcgcaa ccaggcgac 1620
catctgtctg acagcacccc taagcaggtt gaagaagcag gcgacaaact gccgctgac 1680
gacaaaactg ctatcgagtc tgcgctgact gcaactggaaa ctgctctgaa aggtgaagac 1740
aaagcgcgta tcgaagcgaa aatgcaggaa ctggcacagg ttccocagaa actgatggaa 1800
atgcgccagc agcaaatatc ccagcagcag actgcggtg ctgatgtctc tgcacacaa 1860
gcgaagaatg acgatgttgt cgcgctgaa ttgaaagaa tcaaaagcaa aataaa 1917

```

<210> 724

<211> 1647

<212> DNA

<213> Artificial Sequence

<220>

<223> *Escherichia coli*

<400> 724

```

atggcagcta aagacgtaaa attcggtaac gacgctgtg tgaaaatgct ggcggcgcta 60
aacgtactgg cagatgcagt gaaagttacc ctgcgtccaa aaggcgttaa cgtagtctgt 120
gataaatctt tccgtgcacc gaccatcacc aagatgtgtg ttccgtgtgc tegttaaatc 180
gaactggaag acaagttcga aatatgggtt ggcgagatgg tgaagaagat gctctotaaa 240
gcacacgacg ctgcagcgca cgttacccac actgcaaccg tactggtcca ggctatcacc 300
actgaaggtc tgaagaactg tctgcggcgc atgaaccgca tgcactgtac agctgttacc 360
gacaaagcgc ttacgctgtc agttgaagaa ctgaaagcgc tgtcgttacc atgctctgac 420
tctaaagcga ttgctcaggt tggtaaccac tccgctaact ccgacgaaac cgtaggttaa 480

```



```

ctgatcgctg aagcgatgga caaagtcggt aaagaaggcg ttatcacctg tgaagacggt 540
accggtctgc aggcagaact ggacgtggtt gaaggtatgc agttcgacgc tggctacctg 600
tctctctaact tcatacaaaa ccggaagaact ggocgagtag aactggaaaag ccogtctatc 660
ctgctggctg acaagaaaaa ctccaacatc cgcgaatgct tgcccggttct ggaagctggt 720
gccaaagcag gccaaacogct gctgatcatc gctgaagatg tagaaggcga agcgcctggca 780
actctgggtt tttaacacca gctgggcatc gtgaaagtgc ctgcggttaa accgcogggc 840
ttcggcgatc gtgttaaaag tatgctgcag gatatacga cctcgactgg cggtagcgtg 900
atctctgaag agtagcgtat ggagctggaa aaagcaacct aggtcaggct 960
aaacgtgttg tgatacaaaa agacaccacc actatcatcg atggcgtggg tgaagaagct 1020
gcaatccagg gccgtgttgc tcagatccgt cagcagattg aagaagcgac ttctgactac 1080
gacgcgtaaa aactgcagga acgcgtagcg aaactggcag cggcggttgc agttatcaaa 1140
gtgggtgctg ctacogaagt tgaatgaaa gagaaaaaag caogcgttga gatgcctgt 1200
cacgcgaccc gtgctgcggt agaagaaggc gtggttgctg gtgggtggtg tgcgctgata 1260

```

```

cgcgtagcgt ctaaaactgg tgacctgcgt ggtcagaacg aagaccagaa cgtgggtatc 1320
aaagttgcac tgcgtgcaat ggaagctccg ctgcgtcaga tcgtattgaa ctgcggcgaa 1380
gaacgctgct tctgtgtcaa cacogttaaa ggccgcgacg gcaactacgag ttacaacgca 1440
gcaacccgag aataccgcaa catgatcgac atgggtatcc tggatccaac caaagtaact 1500
cgtttcgtct tgcagtcacg agcttctgtg gctggcctga tgatccacac cgaatgcagt 1560
gttacccacc tggcgaaaaa cgtatgcagt gacttaggcg ctgctggcgg tatggcgcg 1620
atgggtggca tggcgcgcat gatgtaa 1647

```

<210> 725

<211> 1935

<212> DNA

<213> Artificial Sequence

<220>

<223> Escherichia coli

<400> 725

```

atggcgaaaa acctaatact ctggctggct attgcggttg tgcgtgatgc agtattccag 60
agctttgggc ccacgcagtc taatggccgt aaggtggatt actotacott cctacaagag 120
gtcaataacg accaggttcc tgaagcgcgt atcaacggag gtgaaatcaa cgttaccaga 180
aaagatagta accgttatcc cacttaccat cgggttcagg atccgaaatt actggataac 240
ctgttgacca agaacgtcaa ggttgcggtt gaacgcgctg aagaaccaag cctgctggct 300
tctatcccca tctcctgggt ccogatgctg ttgctgattg gtgtctggat cttctctatg 360
cgtcaaatgc agggcggcgg tggcaaaagt gccatgtcgt ttggttaagag caaagcgcgc 420
atgctgacgg aagatcagat caaaaacgacc ttgtgctgacg ttgcgggctc cgaacgaaga 480
aaagaagaag ttgctgaact ggtttagtat ctgcgcgagc cgagccgctt ccagaaactc 540
ggcggttaag tcocgaaaag cgtottgatg gtgcgtctcc cgggtaccgg taacacgctc 600
ctggcgaaag cgtatgcagg cgaagcgaaa gttcgtttct ttactatctc cgtttctgac 660
ttcgtgaaa ttgtctcgg tgtgggtgca tcccggttgc gtgaacatgtt cgaacggcgt 720
aagaagcgg caccgtgcat catctttatc gatgaaatgc acgcgtagg ccgcacgcgt 780

```

```

ggcgctggct tggcgctgg tcacgatgaa cgtgaacaga ctctgaacca gatgctggtt 840
gagatggagt gcttcgaagg taacgaagg atcatcgtta tcgcgcgacg taacogtccg 900
gagcttctcg accgcgcctc gctgcgtctg ggccgtttcg accgtcagggt tgtgctggcg 960
ttgcacagat tgcggctcgt tgagcagatc ctgaaagttc acatgcgttc cgttaccattg 1020
gcgcgcgata tcgacgcggc aatcatggcc cgtggttact ctggtttctc cgtgctgac 1080
ctgcggcaacc tgggtgaacga agcgcgcact ttgctgctgc ttgggcaaaa accgctgtgtg 1140
tgaggtgttg agttgcgaaa agcgaaaagc aaaatcatga ggtggtcgga acgctgcctc 1200
atggtgatga cgaagcgcaa gaagaatgc accgcttacc acgaagcggg tatcgtgatt 1260
atcgctcagg tggctgcgga acacgatccg gtgcacaaag tgacgattat ccacagctgt 1320
cgtgcgctgg gtgtgacttt cttcttccct gagggcgacg caatcagcgc cagcgcctag 1380
aaactggaaa gccagatttc tacgctgtac ggtgctcgtc tggcagaaga gatcatctac 1440
gggcgcggaac atgtatatcc cgttgctgcc aacgatatta aactgtgcac gaacctggca 1500
cgttaacatgg tgaactcagt gggcttctct gagaaatgg gtcacactgtc gtaacggaaa 1560
gaagaagtg aagtgttctc cggcgtgac gtacgaaaag gtaacacatg ctccagtgaa 1620
actgcacgta tcatcgacca ggaagtgaag gcaactgatt agcgttaact taactgctg 1680
cgtcagcttc tgaccgcaa tatggatatt ctgcactcga tgaagatgc tctcatgaaa 1740

```

tatgagacta	tcgaacgacc	gcagattgat	gacctgatgg	cacgtcgcga	tgtaactcgc	1800
ccagcgggct	gggaagaacc	aggcgcttct	aacaattctg	gcgacaattg	tagtccaaag	1860
gctcctcgct	cggttgatga	accgcgtacg	ccgaaccggg	gtaacacccat	gtcagagcag	1920
ttaggcgaca	agtaa					1935

<210> 726
 <211> 2673
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Escherichia coli*

<400> 726

atgacagatg	taacgattaa	aacgctggcc	gcagagcgac	agacctccgt	ggaacgcctg	60
gtacagcaat	ttgctgatgc	aggtatccgg	aagtctgctg	acgactctgt	gtctgcacaa	120
gagaaacaga	cttttgattga	ccacctgaat	cagaaaaaatt	caggcccgga	caaatgtacg	180
ctgcaacgta	aaacacgcag	cacctttaac	attcctggta	ccggtggaaa	aagcaaatcg	240
gtaccaatcg	aagtccgcaa	gaaacgcacc	tttgtgaaac	gogattccga	agaggctgaa	300
cgctctgcag	cggaagagca	agcgacgcgt	gaacgcggaag	agcaagcccg	tcgtgagga	360
gaagaatcgg	ctaaacgcga	ggcgcaacaa	aaagctgaac	gtgaggccgc	agaacaagct	420
aagcgtgaag	ctgctgaaca	agcgaaacgt	gaagctgcgg	aaaaagacaa	agttagcaat	480
caacaagacg	atatgactaa	aaacgcccag	gctgaaaaag	cccgcctgtg	gcagggaagct	540
gcagagctca	agcgtaaaag	tgaagaagaa	gcgctgtgta	aactcgaaag	agaagcaact	600
cgogtctgctg	aagaagcaag	tcgtatggcg	gaagaaaaaa	aattggactga	taacgcggaa	660
cgcaactgaag	attccagcga	ttatcacgtc	actactcttc	aacatgctcg	ccaggcagaa	720
gcgaaagcgc	attcgtgaagt	cgaaggcgcg	cgctggccgtg	gtcgtaacgc	gaaagcagcg	780
cgctccgaaga	aagcgaacaa	acacgctgaa	tcaaaagctg	atcgtgaaga	agcagccgca	840
gcgactcgtg	cggtgtaaaag	cggaaaaacgt	aaaggttctt	cgctgcagca	aggtctccag	900
aagcctgctc	agtcgcttaa	cgtgacgttt	gtgatcggcg	aaactatcac	cggtggcgaa	960
ctggcggaaga	gagtcggcgt	taaaagctct	caggtctatca	aagcgatgat	gaaactcgcc	1020
cgaaatcgcaa	ccatcaacca	ggttatcgat	caggaaacgc	caacagctgt	tgctgaagag	1080
atggggcata	aagttatcct	cgctcgtgaa	aacgagctgg	aagagcggtg	aatgagcgac	1140
cgtaacacgg	gtgctgcggc	tgaaccgcgc	gcgcgcgttg	tgaacctcat	gggtcaagct	1200
gacacaggta	aaactctctc	gctggactac	attcgttcaa	cgaaagtggc	ctctggcgaa	1260
gcggcgggcca	taccacgaca	cattggtgca	taccacgttg	aaactgaaaa	cgcgatgac	1320
acctctcctg	acaccccgcg	gcacgcgcgc	tttacttcaa	tgctgtgctg	tggtgcgcag	1380
gcacagagaca	tcgtagtctc	gggtgtgtct	gcgcagcagc	gtgtgatgcc	gcagaccatc	1440
gaagcaatcc	agcacgcgaa	agcgcgcgac	gtaccggtgg	tggtttgcagt	gacaagaatc	1500
gtataaacgc	aagctgatac	ggatcgcgtt	aagaaacgaac	ttccccagta	cgactctcgt	1560
ccggaagagt	ggggcggtga	aagccagtct	gtacacgtat	ctgcgaagac	gggtaccggt	1620
atcgatgaac	tgctggcagc	tatcctgctg	caggcggaag	ttctggagct	gaaagcggta	1680
cgtaaaaggt	tgccgagcgg	tgccggttatc	gaatccttcc	tcgataaagg	tcgtggtctc	1740
gttgctacgc	ttctggttac	tgaaggatct	ctgcacaagg	gcgatatcgt	ctctgtgtgc	1800
ttcgaatacg	gtcgtgtctg	tgcgatcgct	aacgaactcg	gtcaggaagt	gctggaagcg	1860
ggctcogtcca	ttccggtgga	aatcctcgcc	ctgtccggcg	tacogcgctg	gggtgatgaa	1920
gttaccgctt	tacgtgacga	gaagaaagcg	cgtgaagttg	actctatctg	tcagggttaa	1980
ttccgcgaaag	tttaacttgc	gcgtcagcag	aaatctaaac	tcgagaacat	gtctccgcaa	2040
atgcagcaag	tggaagtcca	cgaagtgaat	atcgtcctga	aggcagacgt	acagggttct	2100
gtgcaagcga	ttctcgactc	cttgcgtgaa	ctgtctactg	acgaagttaa	agtggaagtc	2160
alcggtctct	gcgttaggtg	tatcacgcga	acgcagccca	ccctggctgt	ggcgctccaa	2220
gccatcctct	tttgctttaa	cgtacgtgct	gatgcctctg	caagctaaag	gattgaagcg	2280
gaaagcctgg	atctcggtta	ctactccgtc	atctataacc	tgattgacga	agtgtaaacg	2340
gcgatgacgc	gtatcgtctc	tcgggaactg	aaacagcaga	ttatcgtctg	ggcggaagtt	2400
cgtagcgtgt	tcaaatcgcc	gaaatttggt	gccatcgacg	gcatgtatgt	taccggaaggt	2460
gtgggttaaac	gtcacaaccc	gatccgcgtt	ctgcgtgaca	acgtggttat	ctacgaagcg	2520
gagctggagt	ccctgcgcgc	cttcaaatgt	gacgttaacg	aagtcogtaa	cggtatggaa	2580
tggtggtatcg	gcgttaagaa	ctacaacgac	gtccgcgact	gcgattgtat	cgaagtattc	2640
gaaatcatcg	agatccaacg	taccattgct	ttaa			2673

<210> 727
 <211> 2480
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Bacillus anthracis*

<400> 727
 atgaatataa aaaaagaatt tataaaagta attagtatgt catgtttagt aacagcaatt 60
 acctttagatg gtcccgctctt tatcccccct gtacaggggg ogggcggtca tgggtgatgta 120
 ggtatgcacg taaaagagaa agagaaaaat aagaatgaga ataaagagaa agatgaagaa 180
 cgaaataaaa cacaggagaa gcattttaaag gaaatcatga aacacattgt aaaaatagaa 240
 gtaaaaaggg aggaagctgt taaaaaagag gcagcagaaa agctacttga gaaagtacca 300
 tctgatgttt tagagatgta taaagcaatt ggaggaaaaga tatatatgtt ggaatgtgat 360
 attacaaaaa atatatctttt agaagcatta tctgaagata agaaaaaaat aaaagacatt 420
 tattgggaag atgcttttatt acatgaacat tatgtatatg caaaagaaag atatgaaccc 480
 gtacttgtaa tccaattctt ggaagattat gtataaaata ctgaaaaggc actgaaagctt 540
 tattatgaaa taggttaagat attatcaagg gatattttaa gtaaaattaa tcaacocat 600
 cagaaatttt tagatgtatt aaataccatt aaaaaatgc atgattcaga tggacaagat 660
 cttttatttta ctaactcagct taaggaaacat cccacagact tttctgtaga attcttgaa 720
 caaaatagaa atgaggtaca agaagtattt gcgaaagctt ttgcatatta tatcgagcca 780
 cagcatcgta atgttttaca gctttatgca cgggaagctt ttaattacat ggataaattt 840
 aacgaacaag aaataaattct atccttgaa gaacttaaag atcaacggat gctgtcaaga 900
 tatgaaaaat gggaaaaagt aaaaacgcac tatcaacact ggagcgattc tttatctgaa 960
 gaaggaagag gactttttaa aagctgcag attcctattg agccaaagaa agatgacata 1020
 attcattctt tatctcaaga agaaaaagag cttctaaaaa gaatacaaat tgaatagatg 1080
 gattttttat ctactgagga aaaaagattt ttaaaaaaag tacaatttga tattcgtgat 1140
 tctttatctg aagaagaaaa agagctttta atagaatac aggtggatag tactaatcct 1200
 ttatctgaaa agaaaaaaga gttttttaa aagctgaaac ttgatattca acatattgat 1260
 attaatcaaa ggttgcaga tacaggaggg ttaattgata gtocgtcaat taatcttgat 1320
 gtaagaagcg agtataaaag gcatattcaa aatattgatg ctttattaca tcaatccatt 1380
 ggaagtaact ttgatacaaa aatttatttg tatgaaaata tgaatatcaa taaccttaca 1440
 gcaacctcag gtgcgggattt agttgattcc actgataata ctaaaattaa tagaggtatt 1500
 ttcaatgaat tcaaaaaaaa tttcaaatat agtattttcta gtaactatat gattgttgat 1560
 ataaatgaaa ggcctgcatt agataatgag cgtttgaaat ggagaatcaa attatcacca 1620
 gatactcagc caggatatatt agaaaaatgga aagcttatat tacaagaaaa catcgggtctg 1680
 gaaataaagg atgtacaaat aattaagcaa tccgaaaaag aatatataag gattgatgag 1740
 aaagtatgtc caaagagttaa aatagataca aaaaattcaa agcacagtt aaataataat 1800
 caggaatgga atagagcatt agggttacca aaatatcaaa agcttattac attcaacgtg 1860
 cataaatgat cataactcaa tattgtagaa agtgcattat taatttgaa tgaatggaaa 1920
 aataaatctt aaagtgatct tataaaaaag gtaacaaatt acttagttga tggtaatgga 1980
 agatttgttt ttaccgatgt tactctccct aatatagctg aacaatatat acctcaagat 2040
 gagatatatg agcaagtcca ttcaaaaggg ttatatgttc cagaatcccg ttctatatata 2100
 ctccatggag cttcaaaaag tgtagaatta aggaatgata gtgaggggtt tatcaacgaa 2160
 tttggacatg ctgtggatga ttatgctgga tatctattag atagaacca atotgatgta 2220
 gttacaaatg ctaaaaaaat cattgatatt ttaaggaaag aaggagatga ttttaactctg 2280
 ttatggagaa caaattgaagc ggaatttttt gcagaagcct ttagggttaat gactctaacg 2340
 gaccatgctg aacgttttaa agttcaaaaa atgcttcoga aaactttcca atttattaac 2400
 gatcagatta agttcaattat taactcataa gtaactgtatt aaaaattttc aaatggattt 2460
 aataataata ataaataata 2480

<210> 728
 <211> 2295
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Bacillus anthracis*

<400> 728

```

atgaaaaaac gaaaagtgtt aataccatta atggcattgt ctacgatatt agtttcaagc 60
acaggtaatt tagagtgta ttagcagcaa gttaaacagg agaaccgggt attaaatgaa 120
tcagatacaa gttccagggt gttactagga tactatttta gtgatttgaa tttcgaagca 180
cccatgtgtg ttacctcttc tactacagggt gatttatota ttctagtctc tgagttagaa 240
aatattccat cggaaaaacc atattttcaa tctgtctatt ggtoaggatt tatcaaatgt 300
aagaagagt atgaatatat atttgctact tccgtcgata atcatgtaac aatgtgggta 360
gatgaccaag aagtgattaa taaagctctc aattcttaaca aaatcagatt agaaaaagga 420
agattatcat aataaaaaat tcaatatcaa cgagaaaatc ctactgaaaa aggatgtgat 480
ttcaagtctg actggaccga ttctcaaaat aaaaaagaa tgatttctag tgataactta 540
caattgcact aatttaaaaca aaaatctctg aactcaagaa aaaaagcgaag taacagtgtc 600
ggacctgagg ttccagaccg tgacaatgat ggaatccctg attcattaga ggtagaagga 660
tatacctgtt atgtcaaaaa taaaagaact ttcttttcc cgtggatttc taattattoat 720
gaaaagaaag gatttaacc aaataaatca tctctgaaa aatggagcac ggctctctgt 780
cgctacagt atttcgaaaa ggttacagga cggattgata agaattgtc accagaggca 840
agacaccccc ttgtggcagc ttatccgatt gtacatgtag atatggagaa tattattctc 900
tcaaaaaatt aggatcaatc cacacagaat actgatagtc aaacagagaac aataagtaaa 960
aatactctta caagtgggac acatactagt gaagtacatg gaaatgcaga agtgcacgtg 1020
tcgtttcttg atattggttg gagtgtatct gcaggattta gtaattcgaa ttcaagtacg 1080
gtcgcaattg atcatcact atctctagca ggggaaagaa cttgggctga aacaatgggt 1140
ttaaataccg ctgatacagc aagattaaat gccaatatta gatattgtaa tactgggacg 1200
ctccaactct acaacgtgtt accaacgact tctgttagtg taggaaaaaa tcaaacactc 1260
cgacaatta aagctgaagga aaaccaatta agtcaaatat ttgcacctaa taattattat 1320
ccttctaaaa atgtcgccgc aatgcatta aatgcacaag acgatttcc ttctactcca 1380
attacaatga attacaatca atttcttgag ttgaaaaaaa cgaaacaatt aagattagat 1440
acggatacag tatatgggaa tatagcaaca tacaattttg aaaaaggaa agtgagggtg 1500
gatcacggct cgaactggag tgaagtgtta cgcgaatttc aagaaacaac tgcacgtatc 1560
atttttaaag gaaaagattt aaatctgtga gaaaggcgga tagcggcggt taatccctag 1620
gatccattag aacgcactaa accggatatg acattaaaaa aagcccttaa atagcattt 1680
ggatttcaag aaccgattgg aaacttaca tatcaaggga aagacataac cgaatttgat 1740
tttaattctg atcaacaac atctcaaaat atcaagaatc agttagcgga attaaacgca 1800
acataacat atactgtatt agataaaaatc aaattaaatg caaaaatgaa tattttaata 1860
agtagaaca gttttcatta tgatagaatc aacatagcag ttggggcgga tgagtcagta 1920
gttaaggagg ctcatagaga agtaattaat tctgtcaacag agggattatt gttaaatatt 1980
ccaattgata taagaaaaat attatcaggt tatattgtag aaattgaaag taacgaagg 2040
cttaaaagaa ttataaata cagatatgat atgttgaata ttctagtatt accggcaagg 2100
ggaaaaacat ttatagattt taaaaaatat aatgataaat taccgttata tataagtaat 2160
cccaattata aggtaaatgt atatgctgtt actaaagaaa acactattat taatccctag 2220
gagaatggg atactagtac caacgggac aagaaaattt taattcttct taaaaaagcg 2280
tatgatatag gataaa 2295

```

<210> 729

<211> 822

<212> DNA

<213> Artificial Sequence

<220>

<223> Escherichia coli

<400> 729

```

atggcagttg ttaaatgtaa acgacatct ccgggtgct gccacgtagt taaagtgtt 60
aacctgagc tgacacaagg caaacctttt gctccgttc tggaaaaaaa cagcaaatcc 120
gtgtgctga acacaactgg ccgtatcac actggtcata ccgcaagcag 180
ccttacgta ttgttgactt caaacgcac aaagacggta tcccgcgagt tggttgaact 240
gttgatgac attccgaacg ttccgccaac atcccgctgg ttctgtaca agactgtgaa 300
cgccgttaca tcttgccccc taaagccctg aaagctggcg accagattca gtctggcgtt 360
gatgctgcaa tcaaacccgg taacacctg ccgatgcga acatccgggt tggttctact 420
gttcataacg tagaaatgaa accaggtaaa ggccgttcagc tggcaogtgc ttggtgtact 480
tacgttcaga tctgtgtcgt tgatgtgtgt tatgtcaccc tgcgtctgca ttctggtgaa 540
atgogtaaa tagaagcaga ctgcogtgca actctgggoc aagttggcaa tgcgtgacat 600
atgctgcgag ttctgggtaa agcaggtgct gcacgtggc gtgggtttcg tccgaacttt 660
cgcggttacc cgtagaaccc ggtagaccac ccacatggtg gtggtagaag tctgaatttt 720

```

ggtaagcacc cggttaactcc ttggtggcggt cagaccaaa gtaagaagac ccgcagcaac 780
aagcgtactg ataattcat cgtacgtcgc cgtagcaaat aa 822

<210> 730

<211> 4029

<212> DNA

<213> Artificial Sequence

<220>

<223> Escherichia coli

<400> 730

atggttttaact octataccga gaaaaaacgt attogtaaggt attttggtaa acgtccacaa 60
gttctggatg taocattatct cttttctatc cagcttgact cgtttcagaa attattogag 120
caagatctctg aagggcagta ttgtctggaa gctgtcttcc gttccgtatt ccogattccag 180
agctacacgg gtaattccga gctgcaatcc gtcacgtacc gctctggcga accggtgttt 240
gagctccagg aatgtcaaat ccgtggcggt acctattccg caccgctgog cgttaaacgt 300
cgtctggtga tctatgagcg cgaagcgcoo gaagcaccog taaaagacat taaagaacaa 360

gaagtctaca tgggcgaaat tccgctcatg acagacaaag gtaoctttgt tatcaacggt 420
actgagcgtg ttatcgtttc ccagctgcac cgtagtccgg gcgtctcttt tgactccgac 480
aaaggtlaaaa ccaactcttc gggtaaaagt cgtataaac cgctgtatcat ccoattacogt 540
ggttcctggc tggacttoga attogatccg aaggacaaac tgttogtaog tatogacogt 600
cgocgtaaac tgcctgcgac cactattctg ccgcgcctga actacacac agagcagatg 660
ctogaacctgt totttgaaaa agttattctt gaaatccgtg ataacaagct gaagatggaa 720
ctgggtccgg aacgctcctg ttgtgaaacc gcatcttttg acatcgaaag taacoggtaaa 780
gtgtaactga aaaaaggcgg ccgtataact gogcgcaaca ttgocagctg ggaaaaagac 840
cagctcaaac tgatcgaaat ccggtttgag tacaatcgag gtaaaagtgt tgcataagac 900
tatattgatg agtctaccgg ccagctgctg tgcgcagcga acatggagct gagcctggat 960
ctcgtgctga agctgagcca gtctggtaac aagcgtatcg aaaogctgtt cacaacogct 1020
ctggtatcac gccatctat ctctgaaacc ttaoctgtcg acccaactaa ccgacogtctg 1080
agcgcactgg tagaaatcta ccgcatgatg ccgcctggcg agccgcacag tctgtgaaga 1140
gctgcaagcg tgttogagaa octgttcttc tccgaagacc gttatgaact gtctcggttt 1200
ggctgataga agttcaaacg ttctctcgtg ccgcaagaaa tcgaaggttg ccgtatcctg 1260
agcaagaag acatcattga tgttatgaaa aagctcatcg atatccgtaa ccgttaaggg 1320
gaagtgcagt atatcgacca cctcggaacc cgttgatccg gttccgttgg cgaatggcg 1380
gaaaaaccgt tccgctgttg cctggtaact gtagagcgtg ccgtgaagaa gogtctgtct 1440
ctggcgcatc tggataacct gatgcaacg gatattgatc acgcaacgc gatttccga 1500
cgactgaag agttctctgg ttccgaacg cgtctcaagt ttatggaaca gaacacccg 1560
ctgtctgaga ttcacgcaaa acgtgtatc tccgactcg gccacaggcg tctgaacogt 1620
gaacgtgca gcttcgaagt tcgagacgta caccgcact ctaacggtcg cgtatgtcca 1680
atcgaaaccc ctgaaggtcc gaacatcggt ctgataaact ctctgctcgt gtaacgacag 1740
actaaacga actcgttctc tgagactccg tatcgtaag tgacccgacg tctgtgaact 1800
gaagaaatc actacgtgtc tctatcgaaa gaagcgaact agtattcgc cagggogaac 1860
tccaaacttg tcaagaaggg caactctgta gaagaactgg taacttgcg tagcaaggg 1920
gaatccagct tgttcagcgg ccagcaggtt gactacatgg acgtatccac ccagcaggtg 1980
gtatccgtcg tgcggtccct gatcccgctc ctggaacacg atgaagccaa ccgtgcatgt 2040
atgggtcgga acatgcaacg tcaggccggt ccgactctgc gcgctgata ccgctgggt 2100
ggtaactgga tggacactgc tgttgcgctt gactccggtg taactcgctg agctaaacgt 2160
ttggtgtctg ttcaagtctc ggtatgtccc cgtatogtta tcaaaagtta cgaagacgag 2220
atgtatccgg gtgaagcagg tatcgacatc tacaacctga ccaataacac ccgttctaac 2280
cagaaacact gatacaacca gatccgctgt gtgtctctcg gtgaacccgt tgaactgtcg 2340
cagctgctgg ccagcggctc tccaccgac ctccgtgaac tggcgcttgg tcaagacatg 2400
ccgctagcgt gctatccgtg gaatggttac aactcgaag actccatcct cgtatccgag 2460
cgtgtgtctc aggaagacgg tttaaccacc atccacatc aggaactggc gtgtgtgtcc 2520
cgtgacacaa acgtgggtcc ggaagagat accgctgaca tcccgaaagt gggtagaact 2580
gcgctctcca agctgagtag atccggtatc gctcggaagt gcgtcggaag gcagctggc 2640
gacattctgg ttggttaagg aacgcgaaa ggtgaaact agctgacccc agaaagaaaa 2700
ctcgtcgcgt cgtatctcgg tgagaagac tctgaactga aagactcttc tctgacgcta 2760

```

cacaacgggtg  tatccgggtac  ggttatcgac  gttcagggtc  ttactcgcca  tggcgtagaa  2820
aaagcaaac  gtccgctgga  aatcgaaaga  atcgagctca  aacaggcgaa  gaaagacctg  2880
tctgaagaac  tgcagatcct  cgaagcgggt  ctgttcagcc  gtatccgtgc  tgtctgggta  2940
gccgctggcg  ttgaagctga  gaagctcgac  aaactccgcg  gcgatccgtg  gctggagctg  3000
ggcctgcagc  acgaagagaa  acaaaatcag  ctggaacagc  tggctgagca  gtatgcagaa  3060
ctgaacaac  agttcgagaa  gaaactcgaa  cgaaacgcgc  gcaaaatcac  ccaggcgccg  3120
gatctggcac  cgggctgctc  gaagattggt  aaggtatata  tggcggttaa  acgcgctatc  3180
cagcctgggt  caaagatggc  aggtcgtcac  ggttaacaag  gtgaatttc  taagatcaac  3240
ccgatcgaa  atatgcctta  cgatgaaaac  ggtacgcgcg  tagacatcgt  actgaaccgc  3300
ctggcgctac  cgtctcgat  gaacatcggt  agatcctcg  aaaccacact  gggtatggct  3360
tcgaagaagt  tccgcgaa  gatcaacgac  atgctgaaac  agcagcaaga  agtcgcgaaa  3420
ctgcgcgaat  toctocagcg  tgcgtacgat  ctggcgctgc  acgttcgtca  gaaagttgac  3480
ctgagtaact  tcagcgatga  agaagttatg  cgtctggctg  aaaacctcgc  caaaggtatg  3540
caaatcgcaa  cgcggtggt  cgaagctgac  aaagaagcag  aaattaaaga  gctcgtgaaa  3600
cttgccgaac  tgcgcacttc  oggtcagatc  cgcctgtaac  atggtcgcac  tggtagaacg  3660
ttcgagcgct  cggtaacggt  tggttacatc  tacatgctga  taactgaacca  cctggtcgac  3720
gacagatgc  acgcggttc  caccggttct  tacagcctgc  taactgaacca  ccgctcgggt  3780
tactgaagcac  agtctgggtg  tcagcgtttc  ggggagatgc  aagtgtgggc  gctggaagca  3840
gcagcgcgac  ctacacacct  gcaggaaagt  ctacgcgtta  agtctgatga  gctgaaagct  3900
cgtaccaga  tgtataaaaa  catcgtggac  ggcaacctac  agatggagcc  gggcatgcaa  3960
gaatccttca  acgtattggt  gaaagagatt  cggttcgtgg  gtatcaacat  cgaactggaa  4020
gaocgagtaa  4029

```

<210> 731

<211> 4224

<212> DNA

<213> Artificial Sequence

<220>

<223> Escherichia coli

<400> 731

```

gtgaagaagt  tattaaggtt  ttgactcgcc  agaatcgatc  cagactaaaa  cogaagaagt  tgatgogato  60
aaaaattgct  tgccttcgac  agaatcgatc  agaatcgatc  cgttcaggta  ctctcaggta  agttaaaaaag  120
ccggaaacca  tcaactacgc  taacttcgaa  cgaagcagtg  ccggaacgtg  acggcctttt  ctgcgcccgt  180
atctttggcg  cggtaaaaga  ttaacagatg  ctgtcggtga  agtacaagcg  cctgaaacac  240
cgtggcgctg  tctgtgagaa  gtgcggcggt  taacttcgaa  agactaaaag  acgcgctgag  300
cgatattggc  acatcgaaat  ggttcctcgc  gctgcgatgc  actgcgacac  totggttctc  gaaatcgctg  360
ccgtcccgta  tgggtctgct  gctgcgatgc  cgcgtcgctg  actgcgacac  atatcgaaag  cgtactgtac  420
tttgaatcct  atgtggttat  cgaagcggtg  atgacacac  tggaaactgc  gcagatcctg  480
actgaagagc  agtatctgga  cgcgctgga  gagttcggtg  acgaattcga  ccggaagaatg  540
ggggcggaag  caatcagcgc  tctgctgaag  agcatggatc  tggagcaaga  gtgcgaacag  600
ctgcgtgaag  agctgaacga  aaccaactcc  gaaaccaagc  gtaaaaagct  gaccaagcgt  660
atcaaaactg  tggaaagcgt  cgttcagttc  ggttaacaa  cagagtggtg  gatcctgaac  720
gttcctcgcg  taactcgccc  agatctcggt  cgcgctggtc  cgttcggttc  tggctggttc  780
ggcactctcg  acctgaacga  tctgtatcgt  cgcgtcatta  accgttaaca  cgcctctgaa  840
cgtctcgtcg  atctggtgct  gcgggacatc  atcgtacgta  acgaaaaaac  tatgctgca  900
gaagcggtag  agccgctgct  ggataacggt  cgtcgcggtc  gtgcgatcac  cggttctaac  960
aagcgtctct  tgaattcttt  ggccgcagat  atcaaaagta  aacagggctg  tttcgtcaag  1020
aacctctcgc  tgaactactc  tgactactcc  ggtcgttttc  taatcacogt  agttccatac  1080
ctgcgctcgc  atcagctcgc  tctgcggaag  aaaaatggac  tggagctggt  caaaacgctc  1140
atctacggca  agctggaaat  cgcgtgcttc  gatacaacca  ttaaaagctg  gaagaaaatg  1200
gttgagcgct  aagagactgt  cgtttgggat  atctcggacg  aagtattacc  cgaacacccg  1260
gtactcgtga  cactcgcacc  gactcgcacc  cgtcgtggta  tcacagcgat  tgaaccgctg  1320
ctgatcgaa  gtaaaagct  ccagctgcac  cgcgtggttc  gtgcggccta  taacgcgcag  1380
ttcgatgggt  accagatggt  tgttcacgta  ccgctgagtc  tggagcccca  cgtcggaagc  1440
cgtgcgctga  tgatgtctac  caacaacatc  ctgtccccgc  cgaacggcga  accaatcatc  1500
gttcocgtga  aggacgctgt  actgggtctg  tactacatga  ccgctgactc  tgtaaacgcg  1560
aaagcggaag  gaatggctgt  gactggccgc  aaagaagcag  accgtctgta  tcgctctggt  1620
ctggcttctc  tgcattcgcg  cgttaaaagt  cgtatcacgc  agtatgaaaa  agatctgtaa  1680
ggtgaattag  tgcgaaaac  cagcctgaaa  gacacgaatg  ttggcgtgct  atctctgtgg  1740

```

```

atgattgtac cgaaaggctc gccctactcc atcgtcaacc aggcgctggg taaaaaagca 1800
atctccaaaa tctgtgaacac ctgctaccgc attctcggtc tgaaacccgac cggtattttt 1860
cgccgaccaga tcatgtacac cggcttcggc tatgcagcgc ttctgtgtgc atctgttgtt 1920
atcgatgaca tggatcatccc ggagaagaaa caccgaaatca tctccgagggc agaagcagaa 1980
gttgctgaaa ttcaggagca gttccagtct ggtctggtaa ctgcggggcga acgctacaa 2040
aaagtattatc atatctgggc tgcggggaac gatcgtgtat ccaaagcgat gatgggatac 2100
ctgcacaaactg aaaccgctgat taaccgctgac ggtcaggaaag agaaagcaggt ttctctcaac 2160
agcatctaca tgatggccga ctccggtgctg cgtggtctctg ccgcacagat tctcagcttt 2220
gctggttatgc gtggtctgat ggcgaaagccg gatggcttcca tcatcgaaac gccaatcaac 2280
cgcaactctcc gtgaaggtct gaacgtactc cagtacttcca tctccaccoca cgggtgctcgt 2340
aaaggtcttgc cggatcacccg actgaaaaact cgcgaactccg gttacctgac togtcgtctg 2400
gttgactgtgc cgcagggaact ggtggttacc gaagacgatt ttggttaccga tggaggtatc 2460
atgatgactc cgtgtatcga ggttgggtgac gttaaagagc cgtcgcgcga tcgcgtactg 2520
ggtcgtgtaa ctgctgaaag cgttctgaag ccgggtactg ctgatattct cgtccggcg 2580
aaacacgctgc tgcacgaaca gtggtgtgac ctgctggaag agaactctgt cgaacggggt 2640
aaagtacgtt ctgttgtatc ttgtgacacc gactttgggt tatgtgcgca ctgctacgtt 2700
cgtgacactgg cgcgtggcca catcatcaac aagggtgaag caatcgtgtt tatcgcggca 2760
cagtcacatc gtgaaccggg tacacagctg accatcgcta cgtccacat cgggtgtgctg 2820
gcactcgttg cgtgctctga atccagcatc caagtgaaaa acaaaaggtg catcaagct 2880
agcaacgtga agtgggttgt gaactccagc ggtaaaactg ttactacttc cgttaatact 2940
gaactgaaac tgatcgacga attcggttgt actaaagaaa gctacaaagt accttacggt 3000
cgggtactgg cgaaagcgga tggcgaacag gttgctggcg cgcgaaacgt tgcaaaactgg 3060
gaccgcgaca ccactcgggt tatcacgaa gtaagcgggt ttgtactcgt taactgacatg 3120
atcgacggcc agacatttac cgtcagacc gacgaactga ccgtctctgc ttgcgtgtgt 3180
gttctggatt ccgcagaacg tacccgaggt ggtaaagatc tgcgtccggc actgaaaact 3240
gttgatgctc aggggtaaac cgttctgata ccaggttacg atatgccagc gcagtacttc 3300
ctgcggggta aagcgattgt tcagctggaa gatggcgctac agatcagctc tgggtgacac 3360
ctggcgggta ttccgcagga atccggcggt accaaggaca tcaocggtgg tctgcgcgcg 3420
gttgccggacc tgttcgaagc acgtcgtccg aaagagccgg caactcctggc tgaattcaagc 3480
ggttactggtt ccttgcgttaa ggaacccaaa ggttaaacctc gtcctggtat caccocgcta 3540
gacggtagcg atccgtaca gaagatgatt cgcgaatggc gtcagctcaa cgtgttoga 3600
gtgaaacgtg tagaacgtgg tgacgtaatc tocgacggtc cgcgaagcgg cagacacatt 3660
ctgcgtctgc gtggtgttca tgcgtttact cgtttacatc ttaacgaagt acaggaacgt 3720
taccgtctgc agggcgttaa gattaacgat aaacacatgc aggttatcgt tctcagatg 3780
ctgcgtaaag ctacattcgt taacgcgggt agctccgact tcoctggaag cgaacgggt 3840
gaatactcgc cgttcaagat cgcacacccg gaactggaag cgaaaggcaa agtggtgtca 3900
acttactccc cgtatctgct gggtatcacc aaagcgtctc tggcaacoca gtccttcatc 3960
tcccgggcat cgttccagga gaccactcgc gtgctgacgc aagcagcgt tgccgggcaaa 4020
cgcgacgaac tgcgcgctc gaaagagaac gttatcgtg gtctgtgat cccgcaggt 4080
accggttacg cgtaccacca ggatcgtatg cgtcgcgctg ctgcgggtga agctccgctg 4140
gcaccgcagg tgaatgcaga agacgcatct gccactcgtg cagaactcgt gaacgcaggt 4200
ctggcggtt ctgataacga gtaa 4224

```

<210> 732

<211> 3734

<212> DNA

<213> Artificial Sequence

<220>

<223> Concatenation of *S. pyogenes* genes

<220>

<221> misc feature

<222> 499-598, 1049-1148, 1587-1686, 2093-2192, 2652-2751, 3201-3301

<223> n = A,T,C or G

<200> 732

aaccttaatt ggaaagaac ccaagaagtc ggttccgttg ttgaaaaaga attgggcatt 60

ccttttgcca ttgacaaatg tgccaatgtg gtcgccttg gtgaacgttg ggttaggtgt 120

ggtgaaaata accagatgt cgtcttcatg acacttgga caggtgtcgg tggagcatt 180

attgctgatg gtaacttgat tcatgggtgt gcaggagcag gtgggtgaaat cggccacatg 240
 attgtgtgag cagcaaatgg ctttgcttgt acttgtggct cacacggctg tttgggaaaca 300
 gttagcttcag caacaggagtg tgtcaagtg gcacgtttac tggcagaagc ctaocgaagg 360
 gattcagcca tcaaaagcagc tattgacaat ggtgaaggtg ttaccagtaa agacattttc 420
 atggcggctg aagcaggggga ttcccttggct gattctgttg tgggaaaggt tgggttactac 480
 cttggccttg cttcagcann nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 600
 cttacttcga accatgaaac ttttggaagt accaactaag ggacagatta ggtttgaggg 660
 gattgatatt acogataaga agaatagat tttcagcatg cgtgaaaaaa tgggaatggt 720
 tttcagcagc tttcaactct tcccaatat gactatttta gaaataatca ctttctagcgt 780
 aatcaaaaat aaggaagatgg taaagacaga ggctgacaaa acagccttga cgtgtgtgga 840
 caaagtgtgga ttatcagaaa aagcgaaggg ttatctgtct agtcttttga gtgtggcaaca 900
 gcagcggagt gcgattgcgc gtggactggc tatggatcca gatgttttac tctttgatga 960
 accaacttca gctctagacc cagaatgggt ggggtgaggtc ttggctgtca tgcaagattt 1020
 ggctaaatct gggatgacta tgggttattnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1080
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1140
 nnnnnnnngc atgcaatacc gcaacagcgg tggcttgga gaagtaaaaa gcagctttag 1200
 atattcctgt tttggaggtt gctcttacgg gggcagagcg agctattaaa tcaacgacaa 1260
 aaggcaggtg tggggtctac ggaaccccaa tgacagtggtc ttacagacatt tatcgcaaaa 1320
 aaatccagct attagacaca ctatttcaag taaggagctc tgcctggccc aagtttgtac 1380
 cgattgtgga atcaaatgag atgtgttcga gtatagctaa aaaaatgctc ttctatgccc 1440
 tagcaccatt agtcggtaaa atagataccc ttgtactagg atgtactcac tatcccttgt 1500
 tacgaccaat tatccaaaat gttatggggc catctgttaa gctgattgag agtggagcag 1560
 aatgcgtccg agatatctct gtcctannnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1620
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1680
 nnnnnnacct atttaaatcg tttacagaaa ctggctaaaa ttttggcaac ggtgatgtgt 1740
 ttgcaaggtt tagacagctg tgcgtgaaacc aatcatatta tccggccgca gtccaatgat 1800
 aatcatgtga ttaacaattca agaaggtcgt cacgcgttgt ttgaaaaggt 1860
 caggaaataca tttcccaattc tatctctttt gaccaacaga ccagattatca ggtgatatac 1920
 ggctcaaaata ttagctgttaa gtgcacttat atgacacagc tggccttaac gcttatcatg 1980
 gccagatgat gttcatttgt ggctgctgat catgttgatt tacctttatt tgatgcgatt 2040
 tttacgcgta ttggggctgc tgaatgattt atttctgggc aatcaacctt tannnnnnnn 2100
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2160
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2220
 catgaacatc aatcccaaaa caagccgtaa ttgtgtcaac agagaccgtt tatcctatc 2280
 agcaggtcat ggaagtgcga tgccttatag cttgtgtacac tttagctggt atgattatc 2340
 tgtagaagat ttaagaagac tccgtcaatg ggggtctaaa acacaggtc accgaaggt 2400
 gaacccacaca gacgtgtgc aagcaaccac aggaacctct ggtcaaggga tcgcaaatgc 2460
 cgttgggatg gccatggcag aagctcatct agcagctaaa tttacaacac caggtttga 2520
 catcgttgat cactacacat tgcctttgaa tgggtgacgt gaccttatgg aaggggtag 2580
 ccaagaagca caagatgatg caggacattt aaaacttggg aaattggtct tgcattatga 2640
 ttcaaacgac annnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2700
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2760
 ttcaaaaggt agataatttt ttaactcatc aagtgatta ccggttgatg aaagcaattg 2820
 gtaagtggtt tgcctcaaaa tatgctgagg ctggcattac aaaagtgggt acaatogaag 2880
 cttcaggtat tgcacacgac gtaacgctg cagaagcaat ggtattcct atgattttg 2940
 cgaaaaacaca taaaaacatt accatgacag aaggcatttt gacagcagaa gttttattct 3000
 tcactaaaca agtgacgagc acggtgtcta tgcgtgttaa attcctatg aaagaagaca 3060
 aggttttgat tattgatgac tttttagcta atggtcaggg agccaaaggc ttgattgaga 3120
 ttttggctga agcaggtgca caagtgcgtc gcggttggtat tgtgattgag aaacttttcc 3180
 aagatggctg tcgattgatt nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3240
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3300
 nttgcagctg atagccaaag taaagcccaa cttgccatag aaaaaggtgc tttcaagaaa 3360
 gagattgca cgtgctactt tctcagcgt aaaggtgaa ctttactcgt tgatcaagat 3420
 gaatacccta aatttggaa cagagtggtat aagttagcaa agttacgcc tgcttttacc 3480
 aaagatgagg ggacagtaa tgcgtgtaat gcttcaggaa tcaattgatg agcagcgcca 3540
 attttattga tgaatgaaga gaattaggc tccctatttt agctaaattc 3600
 actagttatg caagtgcagg tgtagaccca agtattatgg gctgcggacc aatacctgct 3660
 acgaaaaagg ctcttgcaaa ggtcagctg acaatgtatg acattgattt gatggaaga 3720
 aacgaagctt ttgc 3734

<210> 733
 <211> 288
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Bacillus anthracis*

<400> 733
 atgagtaaaa aacaacaagg ttataacaag gcaacttctg gtgctagcat tcaaaagcaca 60
 atgtgctagtt atggttacaga gtttgcgact gaaacaaatg tacaagcagt aaaacaagca 120
 aacgcacaaat cagaagctaa gaaagcgcaa gcctctgggt ctgacattca aagcacaat 180
 gctagtattg gtacagaatt tgcactgaa acaga cgtgc atgtcgtgaa aaaacaaat 240
 gcacaatcag ctgcaaaaaca atcacaatct tctagtccaa atcagtaa 288

<210> 734
 <211> 1185
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Escherichia coli*

<400> 734
 atgtctaaag aaaagtttga acgtacaaaa ccgcaacgtta acgtcggtag tatcggtccac 60
 gttgacccatg gtataaacacac gctgacccgt gcaatcacta ccgtactggc taaaacctac 120
 ggcgggtgctg ctccgcgact cgaccagatc gataacgcgc ccgaagaaaa agctcgtggt 180
 atcacatca acaacttctca cgttgaatac gacacccga ccgtcacta cgcacacgta 240
 gactgcccg ggcaacggca ctatgtttaa aacat gatca ccggtgctgc gcagatggac 300

ggcgcatcc tggtagttgc tgcgactgac ggcccgatgc cgcagactcg tgagcacatc 360
 ctgctgggtc gtcaggtagg cgttcogtac atcatcgtgt tccatgaacaa atcgacatg 420
 gttgatgacg aagagctgct ggaactgggt gaaatggaa ttcgtgaact totgtctcag 480
 tacgacttcc cggcgacga cactccgac gtctgtggt ctgctctgaa agcgtggaa 540
 ggcgacgcag agtgggaagc gaaaaatcctg gaactggctg gcttccctgaa tctctacatt 600
 ccggaaccag agcgtgcgat tgacaagccg ttctcgtgc cgtatgaaga cgtattctcc 660
 atctccggtc gtggtacggt cgttgaagc cgtgtagaac gcggtatcat caaagtgggt 720
 gaagaagtgt aaactcgttg tatcaaaag actcagaagt ctacctgtac tggcgttgaa 780
 atgttcogca aactcgtgga cgaaggccgt gctggtgaga acgtaggtgt tctcgtgctg 840
 ggtatcaaac gtgaagaat cgaacgtggt caggtactgg ctaagccggg caacctcaag 900
 ccgcacacca agttcgaaat tgaagtgtac attctgtcca aagatgaagg cggcgtcat 960
 actcogttct tcaaaagcta ccgtccgcag ttctacttcc gtaactactga cgtgactggt 1020
 accatgacac tgcgcgaagg cgtagagatg gtaatgcggc gcgacaacat caaaactggt 1080
 gttaccctga tccaccgcgt cgcgatggac gacggtctgc gtttcgcaat ccgtgaaggc 1140
 ggccgtaccg ttggcggcgg cgtttagtag aaagtcttga gctaa 1185

<210> 735
 <211> 2856
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Escherichia coli*

<400> 735
 atggaaaaa catataacc acaagatata gaacagccgc tttacagaca ctgggaaaag 60
 cagggtcact ttaagcttaa tggcgatgaa agccaggaaa gtttctgcat catgatcccg 120
 ccgcgcgaac tcaccggcag tttgatatg ggtcagcct tccagcaaac catcatggat 180
 accatgatcc gctatcagcg catgcaggcg aaaaacaccc ttgtggcagg cgtactgac 240
 caccgcggga tgcctaccca gatggtcgtt gacgcaaga ttgcccgaga agaagtgaa 300
 acccgtaacg actacggcgg cgaagcttct atcgcaaaa tctgggaatg gaaagcgaa 360

```

tctg gcgcca ccattaccgc tcagatgcgc cgtctcgcca actcogtcga ctgggagcgt 420
gaac gcttca ccatggacga aggcctgtcc aagaagtttt cgttcgtctg 480
tata aagaag acctgattca ccgtggcaaa cgctggtaga actgggatcc gaaactcgc 540
accg ctatct ctgacctgga agtcgaaaac cgcgaatcga aaggttcgat gtggcacatc 600
cgct atccgc tggctgacgg tgcgaaaacc gcgacaggtg aagattatct ggtggtcgcg 660
acta ccgcgc cagaaaacct gctggcgcat actggcgtag ccgttaaacc ggaagatccg 720
cgtt acaag atctgattgg caaatatgtc attctcgccg tggttaaacc tctgattccg 780
atcg ttggcg acgaacacgc cgacatggaa aaaggcagcc tgcgctgtaa aatcactccg 840
gcgc acgact ttaacgacta tgaagtgggt aaacgtcac cctcgccgat gatcaacatc 900
ctga cctttg acggcgcatat ccgtgaaagc gccacggtgt tgcataccaa aggttaacgaa 960
tctcagcgttt attccagcga aatccctgca gagtccagga aactggagcg ttttgcgtca 1020
cgta aagcag tctgttcgcg agttgacgcg tctggcctgc tggaaagaaat taacacgcac 1080
gacc tgaccg ttccttacgg cgaacctggc ggctagatta tcgaaacaaat gctgaccgac 1140
cagt ggtacg tgcgtgcgca tgtcctggcg aaacccggcg ttgaagcggt tgagaacggc 1200
gaca ttcagt tctgtaacgaa gcagtacgaa aacatgtact tctcctggat gcgcatattt 1260
cagg acctgt gtatctctcg tcagtttggt tggggtcacg gtatcccgcg atggtatgct 1320
gaag cgggta acgtttatgt tggcgcaaac gaagacgaag tgcgtaaaga aaataacctc 1380

```

```

gggt ctgatg ttgtcctgcg tcaggacgaa gacgttctcg atacctgtgt ctcttctgcg 1440
ctgt ggacct tctctacctc tggctggcgg gaaaataccg acgacctgcg tcagttccac 1500
ccaa ccagcg tgatggatct tggtttcgac atcattttct tctggattgc cgcgatgac 1560
atga tgacca tgcacttcat caaagatgaa aatggcaaac cgacggtgcc gttccacacc 1620
gttt acatga ccggcctgat tctgtgatgc gaaggccaag agatgtccaa atccaaaggt 1680
aaog ttatcg accoactgga tatgttgac ggtatttcgc tgcagaaact gctggaaaaa 1740
cgta ccggca atatgatgca gccgcagctg gcgcgaaaaa tccgtgaagc caccgagaag 1800
cagt tccoga accgtattga gcgcgaacgt actgacgcgc tccgcttcac ctcggcgcg 1860
ctgg cgtcta ccggtcgtga catcaactgg gatataaagc gtctggaagg ttaacgtaac 1920
ttct gtaaca agctgtggaa ccgcacgcgc ttgtgtcgtg tgaacacaga aggtcaggat 1980
tgcc gcttca accggccgga aatgacgctg tgcgtggcgg accgctggat tctggcgagg 2040
ttca accaga ccatcaaaag gtaaccgcgaa gcgtgggaca gcttcgctt cgtatcgcc 2100
cgag gcatca tgtatgagtt cacctggaaac cagttctgtg actggttatct cgagctgacc 2160
aagc cgttaa tgaacggtgg caccggaagca gaactcgccg tctactgcga taocgttggt 2220
actg tactgc aaggtctcgt cgcgcctcgcg catccgatca ttcctgtcat caccgaaaac 2280
atct gcgcgc gttgtaaaat actttcggtt atcactgcgc acaccatct gctgcagcgc 2340
ttcc cgcagt acgatgcac tcaggttgat gaagccgcac tggccgacac cgttcgctg 2400
aaac agggca tctgtcggtt acgtaacatc cgtgcagaaa tgaacatcgc gcggcgcaaa 2460
cogctggagc tgcgtcgcg tggttgcagc gcggatgcag aacgtcgctg aaatgaaaaa 2520
cgtg gcttcc tgcaaaacct gcgcgcgtct gaaagtatca ccgtgctgcc tgcgatgac 2580
aaag gtcocg tttcgtttac gaagatcatc gacggtgcag agctgtgct ccgatggct 2640
ggcc tcatca acaagaaga tgagctggcg cgtctgcgga aagaagtggc gaagattgaa 2700
ggtaaatca gcgctatcgc gaacaaactg gcgaacgaag gotttgcgc ccgcgcacgc 2760
gaag cgtgca tgcgaaaga cgtgagaag ctggaagcct atgcggaagc gaaagcgaaa 2820
cgtattgaac agcagcgtt tatgcgcgcg ctgtaa 2856

```

<210> 736

<211> 1770

<212> DNA

<213> Artificial Sequence

<220>

<223> Escherichia coli

<400> 736

```

atgcgtacag aatattgtgg acagctccgt ttgtccacg tggggcagca ggtgactctg 60
tgtgtgtggg toaacgcgtc tctgtatctt ggtagcctga tcttcatcga tatgcgcgac 120
cgcgaaagga tctgtcaggt atttttogat ccggtatcgt cggacgcgtt aaagctggcc 180
tctgaactgc gtaattgagtt ctgcatcag gtcaaggcca cgtacgctgc gctgacgaa 240
aaaaattatta accgcgatat ggccacccgc gaaatcgaag tctggcgctc ctgcgtgact 300
atcatcaacc gcgcagatgt tctgcgcgtt gactctaaac gactctaaac cgaagacgag 360
cgtctgaatt accgctaacct gcacctcgtt cgtccggaaa tggctcagcg cctgaaaaac 420
cgcgctaaaa taccagcgtt ggtgcgcgct tttatggatg accacgctct cctcgaacatc 480

```

```

gaaactccga tgcgtaccac agccacgcgc gaaggcgcgc gtgactacct ggtgccttot 540
cgtgtgcaca aaggttaaat ctacgcactc ccgcaatccc cgcagttggt caaacagctg 600
ctgatgatgt ccggttttct ccgttactat cagatcggtta aatgcttcgc tgacgaagac 660
ctgcgtgctg accgtcagcc tgaatttact cagatcgatg tggaaacttc ttcatgacc 720
gcgcgcgaag tgcgtgaagt gatggaagcg ctggtgcgtc atctgtggct ggaaagtgaag 780
gggtgggatc tgggcgattt ccgcgtaatg acctttgcgg aagcagaa cg cgttatggt 840
tctgataaac cggatctcgc taaccgcgat gaactgaotg acgttgtct ga tctgctgaaa 900
tcctgtgatt ttgctgtatt tgcaggtccg gcgaacgata cgaaaggtcg cgtagccgct 960
ctgcgcgttc cgggcgcgcg atcgtcgacc cgtaaagcaga tgcagcaaa ta cgttaacctt 1020
gttaaaatct acggcgcgaa aggtctggct taactcaaa g ttaacgaa cg ccgcaaaagt 1080
ctggaagatg tcaacagccc ggtagcgaag ttocttaag cagaatact at gaagacatc 1140
ctggatcgta tgcgcgcgca agatggcgat atgattttct tcggtgcgca caacaagaaa 1200
attgttgcgc acgcgatggg tgcactgcgc ctgaaagtgg gtaaaagact tggctcgacc 1260
gacgaagaca aatgggcacc gctgtgggtt atcgacttcc cgaatgtt ga agacgaaggt 1320
gaaggcgcgc tgaagcgaat gcaccatccg ttacactcac gaaagat at gacggtgca 1380
gaactgaagc cgtcacccga aaatgcggtc gcgaacgctt acgatattgt catcatggt 1440
tacgaagtga cgggtggttc agtaactgac cataatgggt atatgcagca gacggtgttt 1500
ggttattctg gtatcaacga agaggaacag cgcgagaaat tcggttctct cgtcgacgt 1560
ctgaataact cagctccgcc gcacgcaggt gtcttgac cg tctgacatg 1620
ctgctgacgc gaaccgcaca tatccgtgac gttatcgctt ccccgaaa ac cagcggcgga 1680
cgtgtctcga tgaactgaag accgagcttt gctaaccgca ctgcactg gc tgagctgagc 1740
attcaggttg tgaagaagc tgagaataac 1770

```

<210> 737

<211> 3699

<212> DNA

<213> Artificial Sequence

<220>

<223> *Yersinia pestis*

<400> 737

```

atgatggttt tccagccaat cagttagttt ctcttgataa ggaatgcggg aatgtctatg 60
tattttaata aaataatttc atttaattt atttcaagaa tagttatttg tatcttttgg 120
atatgtggaa tgttcatggc tggggcttca gaaaatatg atgtcaacgc acccgcaacag 180
gtccagcctt attctgtctc ttcatctgca ttgtaaaatc tccatctcaa taatgaaatg 240
gagagtccaa tcaatccctt ttccgcacgc gatacagaaa gaaatgctgc aataatagat 300
cgcgcgaata aggagcagga gactgaagcg gtgaataaga tgataagc ac cggggccagc 360
ttagctgcat caggcagggc atctgatgtt gctcaactcaa tgggtggcga tgccgttaat 420
caagaaatca aacagtgggt aaatcgattc ggtaacgctc aagttaatct gaattttgac 480
aaaaattttt gcctaaaaa aagctctctt gattggctgg ctcttggtga tgactctggt 540
tcattctctc ttttttagta gtttaggtatt cgcaataaag acagccgcaa cacacttaac 600
cttgcgctcg ggatacgtac attggagaac ggttggctgt acggaactaa tactttttat 660
gataatgatt tgaccggcca caaccacgt atcggctctg gtgcgcaggc ctggacagat 720
tatttaagct tggctgcoca tgggtatttt cgcctcaatg gatggcact gtcgcgtgat 780
ttctccgact ataaagagcg cccagccact ggggggggat tgcgcgcgaa tgccttattt 840
ctgcactacc gcaactggg ggggaagtg atgtatgagc aatacaocgg tgagcgttgt 900
gctttatgtg ccocagaaa ccccgacta ggtcgggggt tgcagtaaa gc tttagctttt 960
gggtcagtta taanaacccc ttttgatttt ttaaaacagt ttgoggtctg gcaactgcaa 1020
atgttccaaa agaaatccaa agggggtccc aatgagggat gaaaagagct tagcgcacac 1080
ccgatggaac tgtaaatatc atatatgttt tgcgcggaag taccggaagc aggtgttcta 1140
cgggaaaaaa cgcagagcat ttggcaglat ttaagaaaa ttcgcgcat atgcttctgg agtaaaaaag 1200
gaatatcctg gaacgcagat actgtgtgga tcaactccat atgtctctgg agatcccgcc 1260
caagatcgct tgcgcgcat ttatggggtg octgaagga aagagcagta agatgcttta 1320
tgagcagttt ggcgatttga agttcaata ccgttaacag gagttttgt gtcgagggta 1380
ttacgttgtat accgttagga aaaaacagcg caggatataa gaatacata agcaccattt 1440
ggaagaggat aaaaatgggt agcaactctc gatcccgat cccggtagcc cgtttaacgg 1500
ccgttaagta tccatagatg caaatgtcag ctcccgatgc gctgttga gg cgcgcgctgg 1560
taacagagcc ttatagggcg atatgaaaa atcccgcta tgccggagga tgcgggagga 1620
ggtaaagata atctgcacag caacccttat cgcgtgactg cggggtacaa ttacaccccc 1680
gtgcctctac tcactgtgcg ggtagatcag cgtatgggga aaagcagt aa gcatgaaaca 1740

```

cagtggaacc	tccaaatgaa	ctatcgccctg	ggcgagaggtt	ttcagtcgca	acttagccct	1800
tcagcggttg	cggaacacg	tctactggct	gagagccgct	ataaccttgt	cgatcgtaac	1860
aataatatcg	tgttgtagta	tcagaaacag	caggtgggta	aactgacatt	atcgccagca	1920
actatctccg	gctcgccggg	tcaggtttat	caggtgaacg	cacaagtaca	aggggcact	1980
gotgtaagg	aaattgtctg	gagtgatgcc	gaactgattg	ccgctggcgg	cacattaaac	2040
ccactgagta	ccacacaati	caacttggtt	tlaccgcctt	ataaacgcac	agcacaagtg	2100
agtccggtaa	cggaacgacct	gacagccaac	ttttattcgc	ttagtgcgct	cgcggttgat	2160
caccaaggaa	acagatctaa	ctcattcaca	ttgagcgctc	ccgttcacga	gcctcagttg	2220
acattaacgg	cggcgcgtcat	tggatgatgc	gcaccggcta	gtgggaaaaa	tgcaatcac	2280
gttgagtcca	ccgtgtctga	ttttgagggg	aaacccttag	ccgggcagga	agtggtgata	2340
accaccaata	atggtgcgct	accgaataaa	atcacggaaa	agacagatgc	aaatggcgct	2400
gcgcgcattg	catttaacaa	tacgcagat	ggcgtagcgg	tagtcaacg	agaagtggag	2460
gggcaacggc	aaagtgttga	taccocacttt	gttaagggta	ctatcgcgcc	ggataaaacc	2520
actctggctg	cggtaccgac	atctatcatc	gctgatggtc	taatggcttc	aaccatcacg	2580
ttggagtgtg	aggataccta	tggggaccgc	caggctggcg	cgaatgtggc	ttttgacaca	2640
accctaggca	atatggcgct	tatcacggat	cacaatgacg	gcacttatag	cgccaccattg	2700
accagtacca	cggtgggggt	agcaacagta	acggtgaaa	tggatggggc	tgogttcagt	2760
gtgcgcagtg	tgacggttaa	tttcacggca	gatcctattc	cagatgtcgg	ccgctccagt	2820
ttcaccgctc	ccacaccgga	tatcttggct	gatggcacga	tgaattccac	attatccttt	2880
gtccctgtcg	ataagaatgg	ccattttatc	agtgggatgc	agggccttag	ttttactcaa	2940
aacggtgtgc	cggtgagtat	tagccccatt	accgagcagc	cagatagcta	taccgcgacg	3000
tggtgtggga	ataccgcggg	tgatgtcaca	atcacgcctc	tggttgatac	cctgataactg	3060
agtaacttgc	agaaaaaaat	atccctattc	ccggtaccta	cgctgaccgg	tattctggtt	3120
aacgggcaaa	atctcgctac	ggataaaggg	ttccggaaaa	cgatctttaa	aaacgccaca	3180
ttccagttac	agatagataa	cgatgttgct	aataaatact	agatagtgta	gtcgctgtca	3240
ttcacaccca	atgtatcggt	taacgatcag	ggtcagggtg	cgattaccta	ccaaacctat	3300
agcgaagtgg	ctgtgacggc	gaaaagttaa	aaattcccaa	tttatctcggt	gagttatcgg	3360
tctcacccaa	atcgggtgga	atcacgatgc	acactctcgc	gtgatggccc	tgcagaggcc	3420
agcagacaat	gcgaagggtc	agatatgtct	gcggttcttg	aatcctcacg	tgcaacccaac	3480
ggaacgcgtg	cgctcagtcg	gacattgtgg	ggcgatgtgg	ggagcttgac	cgcgatagct	3540
tctgatctgc	aatctgcgga	atattgggtc	aaaagaccga	gcaaggattt	tgaaacccat	3600
aatatgaaca	ctggcctgcg	gcacaccagg	cctgcatact	tggcgttccc	gctctgtgcg	3660
ctgtcaatat	aaccagataa	cagatagcaa	taagaacag			3699

<210> 738

<211> 3891

<212> DNA

<213> Artificial Sequence

<220>

<223> Clostridium botulinum

<400> 738

atgcaatttg	ttataaaca	atttaattat	aaagatcctg	taaatgggtg	tgatattgct	60
tatataaaa	ttccaaatgt	aggacaaatg	caaccagtaa	aagcgtttta	aattcataat	120
aaaatatggg	ttattccaag	aaagataaca	tttacaacac	ctgaagaagg	agattttaat	180
ccacaccacg	aaacaaaaa	agttccagtt	tcatattatg	atccaacata	tttaagtaca	240
gataatgaaa	aagataatta	tttaaaagga	gttacaacaa	tatttgagag	attttatcca	300
actgatcttg	gaagaatggt	gttaacatca	atagttaagg	gaataccatt	ttggggtgga	360
agtcaacaatg	atcacagaatt	aaaagttatt	gatactaatt	gtattaatgt	gatcaaccca	420
gatgggtagtt	atagatacga	agaacttaac	ctagtataaa	taggaccctc	agctgatatt	480
atacagtttg	aatgtaaaaa	ctttggacat	gaagttttga	atcttacggc	aaatggttat	540
ggctctactc	aatacattag	atttagccca	gattttacat	ttggtttttg	ggagtcaact	600
gaagttgata	caaatcctct	tttaggtgca	ggcaaatgtg	ctacagatgc	agcagtaaca	660
tttagcacatg	aacttatata	tgctggacat	agatttatag	gaatagcaat	taatccaaat	720

aggggtttta	aagtaaatac	taatgcctat	tatgaaatga	gtgggtttga	agtaagcttt	780
gaggaactta	gaacatttgg	gggacatgat	gcaaaagtta	tagatagttt	acaggaataac	840
gaatttcctgc	tattattata	taataagttt	aaagatatag	caagtacaact	taataagctt	900
aaatcaaatg	taggtactac	tgcttcatta	cagtatatga	aaaatgtttt	taaaagataa	960
tatctcctat	ctgaagatac	atctggaaaa	ttttcgttag	ataaattaaa	atttgataag	1020

```

ttatacaaaa tgttaacaga . gatttacaca gaggataaatt ttgttaagtt ttttaaagta 1 080
cttaacacaga aaacataatatt gaatttttgat aaagccgtat ttaagataaaa tatagtagcct 1 140
aaggtaaaatt acacaaatata tgatggattt aatgtaagaa atacaaatttt agcagcaaac 1 200
tttaattgttc aaataacacaga aatttaataat atgaattttta ctaaaactaaa aaatttttaact 1 260
ggattgttttg aaattttataa gtgctatgt gtaagaggga taataacttct taaaactaaa 1 320
tcatttagata aaggatacaa taaggcattta aatgatttat gttatcaaat taataattgg 1 380
gaactgttttt ttatgctcttt agaagataat tttactaatg atocataata aggagaaagaa 1 440
atacatctg atactaatat agaagcagca gaagaaaata ttagtttaga tttatcaaaa 1 500
caattattatt taacottttaa ttttgataat gaacctgaaa atattttcaat agaaaattctt 1 560
tcaagtgcaca ttataggcca attagaacct atgcttaata tagaaagatt tctcaattgga 1 620
aaaaaagatag agttagatata atatactatg ttcoatttato ttctgtgcoca agaatttgaa 1 680
caatggtaaat ctatggctttt tttaacaaat totgtttaaag aagcatttatt aaatcttagt 1 740
cgtgttttata cattttttttt ttocagactat gtaaaagaaag ttaataaagc tacggaggca 1 800
gctatgttttt taggctgggt agaacaatta gtatatgatt ttaccgatga aactagocaa 1 860
gtaagtacta cggataaaat tcggcgatata actataatta ttccatatat aggacotcgt 1 920
ttaaattatag gtaattgtgtt atataaagat gattttgtag gtgctttaat attttcagga 1 980
gotgttattc ttgttagaatt tataccagag attgcaatac ctgtattagg taacttttga 2 040
cttgtatcat atattggaaa taaggttcta acogttcaaa caatagataa tgctttaagt 2 100
aaaagaaatg aaaaatggga tgaggtctat aatatatag taacaaattg gttagcaaat 2 160
gttaattcac agattgatct aataagaaa aaaaatgaaag aagctttaga aaatcaagca 2 220
gtagcacaac aggcctataat aaactatcag tataactaat actactgaga agagaaaact 2 280
aatattcaatt ttaattattga tgatttaagt tcgaaactta atgagttctat aaataaagt 2 340
atgattcaata taaataaaatt ttgtaataaa tgotctgttt caattttat gaattctatg 2 400
atocotttatg gtgttaaaag gttagaagat ttgtgatgcta gttctaaaga tgcattatta 2 460
aagtatatat atgataatat aggaacttta attggtcaag tagatagatt aaagataaaa 2 520
gttaataata cacttagtac agataaact ttccagcttt ccaataactg agataatcaa 2 580
agattattat ctacatttac tgaattatatt aagaatatta ttaatacttt tataattgaat 2 640
ttaagatag aaagtaatac ttaatatagac ttacttaggt atgcaatcaa aataattatt 2 700
ggtagtaag taaattttga tccaatagat aaaaatcaaa tcaattatt taatttagaa 2 760
agtagtaaaa ttgaggttaat tttaaaaaat gctattgtat ataatgtat gtatgaaaat 2 820
tttagtacta gcttttggat aagaattcct aagtatttta acagtaataa tctaataat 2 880
gaatatacaa taataaattg tatggaaaat aattcaggat ggaagaaatg acttaattat 2 940
ggtagaaataa tctggccttt acaggatact caggaaaataa acaaaagagt agtttttaaa 3 000
tcagatocaa tgattaatac atcagattat ataaacagat ggtattttgt aacttactc 3 060
aataattagat taaataactc taaaatttat ataaattgaa gattaataga tcaaaaacca 3 120
atttcaaat taggtaatat tcatgctagt aataataata ttgtttaaatt agatggttgt 3 180
agagatacac atagatatt ttggataaaa tattttaatc tttttgataa ggaattaaat 3 240
gaaaaagaaa tcaaagatat atatgataat caatcaaat caggtatttt aaaagacttt 3 300
tggttggtgatt atttcaata tgaataacca tactatatgt taaatttata tgatcocaat 3 360
aaatatgtcg atgtataataa ttgaggtatt agaggttata tgatctttaa agggcctaga 3 420
tgtagctgaa tgactacaaa cattttattta aattcaagtt gtatagggg gacaaaaatt 3 480
attataaaaa aatatgtctc tggaataaaa gataaatttg tataaataaa tgatcgtgta 3 540
tatattaatg tagtagttag aataaaagaa fataggttag ctactaatgc atcacaggca 3 600
ggogtagaaa aaataactaag tgcattagaa atacctgatg taggaaatct aagtcaagta 3 660
gtagtataga agtcaaaaaa tgatcaagga atacaataa atgcgaaat gaatttaca 3 720
gataaataag ggaatgatat aggttttata ggatttcac atgtttataa tatagctaaa 3 780
ctagtacaa gtaatttggt taatagacaa atagaaagt agttaggac ttgtgggtgc 3 840
tcatgggaat ttattctcgt agatgatgga tggggagaaa ggcactgta a 3 891

```

<210> 739

<211> 9047

<212> DNA

<213> Artificial Sequence

<220>

<223> *Staphylococcus aureus*

<400> 739

```

aagcttcttg tgaaaaata tottcaatct tatgaagat ctccacatta tggotaactt 60
ttgagacaa tggttttcca atttcaacog ctcccccatt tgcaccaaga tacaattgat 120
tattaaat aagccacga ccaatacct tatgtatac taagaacga agattattgt 180

```

aggataaatt atgattaaaa ttacgttcat ataacgctga aagattcgct tcattttcaa 240
 ctacgactgg aacatttagta atttctttta ttttcttagc aattgaaatt ccttcagttt 300
 catggaagtg taaattatgct acatgcgtgc cattatccac atagaaacag 360

acacacctaa tagtcggtta taagtatcaa gtttctcctg aatatcaata tgttttttta 420
 ttatgctttaa tatatactaa acccttttcat caggttaaat c ataagattca tgccttaata 480
 cattaccact aaaaataatt tacatcactt caacagaaat ataagttaaa tccaagaaa 540
 aaaaataacc ataaagatga ttaaccttca gaagaatagc ttttttccaa cactctcttg 600
 tgcctatcacc ctccacaaacc tcattatacaa gagatttata cttaaactta ttaaaaatac 660
 tagaaatcgt tgccttatta actcttttaa gatattttga ctcgaaatatt tatgatggtta 720
 taaatttccc tttagcactct ttttttaata tcatttatac tttattttcc ataatgtcct 780
 accocataag ttattttgaa tttagtttat agtttatact tttattttat accaatgctt 840
 ttaacataaa ttaaaattaaa ccttagaaca acttaaaacc tcacttaggt tatcatcttc 900
 gttcttttat tttttttatt atttcaataa attacgtatt tccaatatga cgatttttta 960
 tgcaaaagtc ttgtatgttt ttcaaatatt tgacatttat gcaattcaaa tagcacaata 1020
 gggatatttt aacatttttt atttggttga tattatactt aatgtatctt aaatgaaaag 1080
 aggtatgcat atggtattca ctgggtgtat tacaagcatt attgatttta tcaagacttg 1140
 catcagggct ttcgggttaatt tttttcaact aaaaaacaga ggaatatatt aacgacttta 1200
 ttgtttcttc tgtttttcat gtattgttgt aaaaacacaa tttttatttt ttattcaata 1260
 tattttctca tttctctatt tcatcttggt atagatcttc tttttctaca aagttaaaga 1320
 caagtgaatt gaaacgcgct ttgtataact tattgtataa ttttttagat ttgtttatct 1380
 ttatatcaact tttcttaca agagagtaatt attgaaaaat ttatttgtct tttttagcct 1440
 ctataaactc ctttttatcc aatctcggtta taagtctacg aatggttcct ggaactccagt 1500
 ccttttgcat ttgtattttt ctattatata tattcgcaat tgcataattt ttcatccaaa 1560
 tgatattcat aacttcccat tctgcagatg atatttcaata gcttttata ttcatattat 1620
 taattccatt ttttttaaaa taogctcaga aatttgttgt gctttttcgc catttcgcatt 1680
 gtctctgcct tttaaatgtt tagcaaaaaa atacgtatta tctttcgttt caacataacc 1740
 tacgaacct caattgtctt ctttgtgatt caogattcct ttccagattt tactacata 1800
 ttataaattg tcttttttgt tcaaaatcat actattttca actttttcaa tagcatttt 1860
 atcaaaatga atgttttgtt ttctcatatt tttaacaaaa tttaacctgt ctatgtcaga 1920
 aatttttaat gaagattcat tccaataatt ttoactccct gatattttct cattacocata 1980
 ttcaattaga tctaaataag atttaacctc atctgtctct aaatgtttgt ttaatttttc 2040
 gtaataccga tttaactgaat atttcattga agaattttaa ttttgatctt ggtttccattc 2100
 ttaataccga tattgatggt tatccacttg ttgttcagta tgattttaat agagtaattt 2160
 ttgtgtgaat gcaattaaog ctaaaataat ttgttaagta gaattaggtg aatatcgttg 2220
 tttaacttct ggttcaattat aaatagaata agcttgcctc cgttcaattt aaagcaaaa 2280
 acttccatca aatcctttga aatacggagc tagttgattt aattttttat atgatacatt 2340
 tgttttctat ttgtcttggt gaacatgtgc agatagtaac ggtgcttgta ttaaaagcga 2400
 tatactcaat acatatacag caacaataog cttgtttcga ttagggttag gcattgaatc 2460
 ataaagtcca atataactta acaggttcttt aatatttgaa ttaaaaccta tgaatatattg 2520
 tgcctgccaa ttattttagt gctgagattg taaaatagag catatttata tgcattcaac 2580
 atacagtata ttgttcattgc gattcacaatt tttaaaacag ttctctatcac atacttttct 2640
 acagctattg tccatcattg ttttacttat atatagtgca ggattaaaoc agaattatct 2700
 tttaaaaaaa acataaagct ggttgaatat taagtcatga ctttccatcat gctgatagtc 2760
 atgtagaata atatatccaa ttctcttgct attcatggtt tgcactacga cagttaggtg 2820
 tacaatttgg gatttccata aacocaaatc catcggatta ccaattgttg aacataaact 2880
 aattgttata tgccttttgt agaaactgcat cttactttga catactttaa gtctgttact 2940
 aagatatgac gattccaatg acgaactttt aataacatca attgtcoga atgcttcaat 3000
 catataaaat aagcacacaa aactacocaa taccatattc aaaaagatac tatagcttat 3060
 atttgagttg tcaaaactgat taacattaat tgcataacag atgattgttg 3120
 accctatcac atatgactaa ccgaagaagt cgtgtcagat acaatttcgat tctcatatc 3180
 ttttgaatt gaaaattctg atattttgta aatgggtatt attggaatt acgtggagac 3240
 gagcactaat aaccaaatct tatgtgacat aatattttga gtatatttta tatagagact 3300
 tctccataaa aaaaattacac atatogtgag caatgaaact attataccta catataaaaa 3360
 agatgataac accttctaca cctccatctc acaaaaatta taacattatt ttgacataaa 3420
 tactactatt gaaatatact acaaattgag tcttatataa gaggatattt gatgaaaaag 3480
 ataaaatttg tcccaacttat ttaaatagtt gtatgttgcg ggtttggtat atatttttat 3540
 gcttcaaaag taagaanaat taataact acttgatgaa ttgaagataa aaatttcaa 3600
 caagtttata aagatagcag ttatatttct atgggtgaat atgggtgaat agaatgact 3660
 gaacgtccga taaaatatata taatagttta ggcgttaagc atataaacat tccaggtact 3720
 aaaaataaaa acgtattccta aaataaaaaa cgagttagtg ctcaataata aactaaaaa 3780

aactacggta acattgatgc caacgttcaa ttttaattttg ttaaagaaga tgggtatgtg 3840
aagttagaatt gggatcatatg cgtcattatt ccagggaatgc agaaagacca aagcatatcat 3900
taaaataattg taataatcaga acgtggtaaa attttagacc gaacaacatg gaacttgccc 3960
aaatcaggaaa cacatatgag attaggatc gttccaaaga atgtatctaa aaaagattat 4020
aaagcaatcg ctaagaagct aagtatttct gaagactata tcaacaacaa atggatcaaa 4080
attgggtgaca agatgatacc ttogttccac tttaaaaacog ttaaaaaaat ggaatgaat 4140
ttaagtgtatt tgcgcaaaaa atttcatctt acaactaaatg aaacagaaga tcgtactat 4200
cctctagaaaa aagcgaacttc acatctattta ggttatgttg gtccccatga cctcgaagaa 4260
ttaaaaacaaa aagaatataaa aggcataaaa gatgatcgag ttatttgtaa aaagggactc 4320
gaaaaactttt acgataaaaaa gctccaaact gaagatggct atcgtgtcac aatcgttgac 4380
gataattagca atacaaatcgc acatacattta atagagaaaa agaaaaaaga tggcaaatg 4440
attccaactaa ctattgatgc taaaagttcaa aagagttttt ataaacaact taataaatgat 4500
tatggctcag gtactgctat ccaacctcaa acaggtgaa atattagcact tgtaagcaca 4560
cctctaatatg acgtctatcc atttatgtat ggcattgagta acgaagaata taataaatga 4620
acogaagata aaaaagaacc totgtctcaac aagttccaga ttacaacttc accaggttca 4680
actcaaaaaa tattaaacga aatgattggg ttaataaaca aaacattaga cgtataaaca 4740
agttataaaaa tcatgtgtaa aggttggaac aagataaaat ctgggggtg ttacaacgtt 4800
acaagatgat aagtggttaaa tggtaatatc gacttaaaac aagcaataga atcatcagat 4860
aacattttct ttgctagagt agcaactcga ttaggcagta agaaatgtga aaaggcagt 4920
taaaaactag gtgttggtga agatatacca agtgattatc cattttataa tgcctaaatt 4980
tcaaaaacaaa atttagataa tgaatatatta ttacgtgatt caggttacgg acaaggtgaa 5040
atactgtatta acccagtaca gatcctttca atctatagcg cattagaaaa taatggcaat 5100
attacaogcaa ctcaactatt aaaaagacog aaaaacaaga ttgggaagaa aatatattgt 5160
tccaagaagaa atatcaatct attaaatgat ggtatgcac acgtcgtaaa taaaacacat 5220
aaagaagata tttatagatc ttatgcacaa ttaattggca ttactgtgca tgcagaaact 5280
aaaatgaaac aaggagaaag tggcagacaa attgggtggt ttatatcata tgaataaagt 5340
aatcaaaaaa tcatgatggc tattaatgtt aaagatgtac aagataaagg aatgggtagc 5400
tacaattgcca aaatctcagg taagtgatgat gatgagctat atgagaacog attgaaaaaa 5460
tactgatgat atgaataaca aaacagtga gaaatccgta acgatgggtt cttcaactgt 5520
ttattatgaa ttattataaa gtgctgttac ttctccctta atacaacttt tctcaatttt 5580
attgtatgtt gaaagtgaac ctgtaacagc tccattttct ttttttatgg attttctatt 5640
tgaattttca cgcgataacgt acaatgtatt acotgggtat cagggtttaa taaatttaac 5700
gttattcatt tgtgttccgt ctacaacttc ttctcgttat ttactccttt ctacccataa 5760
tttaaatgat attgaaagt gtatgcacgc agatgcaagt aaagtgtttt caactctttg 5820
ttctgctttt tcttttacta tatgcataa ttgaggaatc ttgttttgat gtttctctga 5880
aatttctctt tctgtaatat gaaggtcttt ttgttttgat gtttctctga atataaaatc 5940
atogtatttc atatatgtct ctctttctta ttcaaatcaa ttttttagta tgtaaacagt 6000
taaaagtgag tctacogtca ctgaaaagta agactcactc ctcaactttct attagagcaa 6060
atgcaccatt ttactgcatt tgtctgtaaa gataccatca actccccaat tagcagaattg 6120
gtttgcacgt gctgggttgt ttacagtcca taactgtcaa tcaataaccog tctctttac 6180
catttttact ttgtcttaag taagtttgcg attctcagtg tttaactatt tagctatttc 6240
gtaatctaaa agtgttctoc agtcttcacg aaacgaagt gtatggaaat taactgtctc 6300
gtatatattg ggcagtgatt ctctgcgaag tttaacaagc gaacacttaa agcttaagt 6360
agctotcttt gattctgat taagtttgtt aattgttctt ccacttgctt aaccatactt 6420
ttagaagtgt ctagtccatt oggtccagta atacctttta attctcacta taactcttga 6480
ttatatctcat ttgctatttt taactacatc tggaaagtgt gcaaatgttc atctttcata 6540
ttttcccaa accaagatcc tgcagaagca totttaattt catcataatt caattcagtt 6600
atttccocgg acatatattgt agtccgtct atcaactcc aactcagttg aatcagttgt 6660
tcatcttttg taattgcaac atcaactcc aaccagttt tacctttcac ttctgaagca 6720
gcttttaaat gtgcaattgt attttcoga gctttactag gcttaactct atgtcaatt 6780
acagttagca tattcaactct ocltgcattt tattttttca attaaogtaa ctgtattata 6840
caacttaogt caacttttatt tccattaaaa agagatgat atcataaata aagaagctga 6900
tagattogta ttgatattag agttaatcta ogctcactc cattttttaa aaatcaatta 6960
tgactccaaa gctccatttt gtaatcaagt ctagttttct tgtacocctt atctgcaatt 7020
ttacttagga ttgcttttaa cttaaccctt atcagaattt taactgagaac tgcttttaac 7080
gatcacctct tatctgcaat ttgctcact acgtgctga atctgttata tatctgttat 7140
tttaactgaga actgttttta acttaaccct tatcagcaat ttgtcagga attgtttta 7200
acgtactctt tactctcaat tttaactgaga actgtttta taaacactct tatctgcaat 7260
tttaacttaga actgttttta agtcaactct taactgttaa tttaactgag aatcgttttt 7320
aacaacactc ttatctgcaa tttaacttag aactgttttt ttatctgcaa ttatctgcaa 7380
ttttactag aattgtcttt actattctct ttattagtat taactcagta agaatcgcta 7440

taaaaatgaa	aattacaacc	gatttttgtaa	gtctggacgc	ctgagggaat	agtatgtgcg	7500
agagactaat	ggctcgagcc	ataccocctag	gcaagcatgc	acgtacaaaa	tcgtaaagata	7560
aaaaaataag	catatcactg	taaacctttaa	aaaatcagtt	tagtgatatt	cttatttatt	7620
tcgagtttag	atttatgtcc	caagctcctc	aagcaccaatc	ggccactagt	ttattttctc	7680
atcttatatg	ttctgatatg	gtcttctata	ctgtataagt	aTacttttga	atatgggatc	7740
tgtgtcoatt	caogttogaa	atcaaatctc	tgattatcaa	atgctgttaa	agaatgttcc	7800
gtattctctg	actgataatt	gcctctcaga	ttctagcata	tttaaagtgt	tctctttatc	7860
taatgtcttg	tcatatcctt	taacgattga	accactaaag	atttctccta	ctgctctcga	7920
accataacta	atagacata	cttctctctc	ggttggaatg	tgtgtgtctg	taataacgaa	7980
attaaaotcta	agttataatga	tctgtataaa	atgttaccaa	catctctatt	gtctcattacg	8040
gttctgttgc	aaagtTgaat	ttatagtata	attttaacaa	aaaggagctc	tctgtatgaa	8100
ctatttctga	tataacaact	ttacaacgga	tgttataoct	gtagcccttg	gctactatct	8160
aagatatata	tttagttatc	gtgatatctc	tgaatatatta	agggaaacctg	gtgtaaacctg	8220
tcatatctca	acggtctacc	gttgggttca	agaatatgcc	ocaaattttg	atcaaaattg	8280
gaagaaaaag	cataaaaaag	cttattacaa	atggogtatt	gatgagacgt	acatcaaaaat	8340
aaaaggaaaa	tggagctatt	tatatogtgc	cattgatgca	gaggggacata	cattgatgat	8400
ttgtgttgcg	aggcaacgag	ataatcattc	agcatatgcg	tttatcaaac	gtctcattaa	8460
acaatttgg	aaactctaaa	aggtaatc	agatcaggca	occtcaacga	aggtagcaat	8520
ggctaaagta	attaaagctt	ttaaacttaa	acctgaactgt	cattgtcatc	cgaaatctct	8580
gaataacctc	tttagcgaag	atcacccgtc	tattaaagta	agaaagacaa	gggtacaaag	8640
tatcatactca	gaaagaata	ctttaaaagg	tattgaatgt	atttacgcctc	tatataaaaa	8700
gaacccgagg	tctcttcaga	tctacggatt	ttcgccatgc	caocgaattc	gcactatgct	8760
agcaagttaa	gcgaacactg	acatgataaa	ttagtgggtta	gctatatattt	tttactttgc	8820
aacagaacgc	aaaaataact	cttcaattta	tttttatatg	aatcctgtga	ctcaagattg	8880
taatatctaa	agatttactg	tcatcataga	caattgtctt	ttcaacattt	tttatagcaa	8940
attgattaaa	taatttctct	aatttctccc	gtttgatttc	actaaccatag	attatatatt	9000
cattgatata	gtcaatgaat	aatgtacaaa	ttatcactca	taacagt		9047

<210> 740

<211> 1832

<212> DNA

<213> Artificial Sequence

<220>

<223> *Acinetobacter baumannii*

<400> 740

cgctgtacg	taatactggt	gaagccccc	gtcctaagac	gatgtttgag	ccagggtgaag	60
aattactgtg	tattgacggt	ccattccacg	actttaaagg	tgtgtgtgga	gagggtcaaat	120
acgaataatc	acagtttaacg	ttgacgatta	acgtgtttta	tcgaccaaat	ccagggtgaac	180
tcgaatttct	ccaagtcgaa	aaaacgattt	aatcttaatt	ggttgaaaag	ccgcgatttt	240
tatcgggcat	tgttgttcta	acagttattg	tacgtagaaa	ttggggagcc	taacggcggt	300
tgtaccacga	ggatcttttaa	atggcctaaga	agattgacgg	ctatatcaag	gtccaaagtc	360
cagctggtaa	agcaaatoca	totccacoga	ttggtcctgc	actaggtcaa	cgtggtgtaa	420
acatcatggc	gttctgttaa	gaattccaaa	aacaatttaa	agttcctacg	gctaaacctc	480
taccagaact	accaagtttt	acggggcgct	tgggtgggta	tttgggctac	gatgctgtcc	540
gctacatcga	gccacgttta	aagaatgtac	ctggggctga	tcagattacg	ctgcacagtt	600
tatgggttat	gctctcaaa	acagtcattg	tttttgaaa	ctttaaagat	acgctatttt	660
taattgtgca	tgcagctaca	gagcagagta	atgcttatga	agacgcgtca	caaaaaattag	720
atacaattga	acagttgttg	gcgactccag	ttagtttgca	agcgctccca	catacgcctc	780
cgcattttga	atcaaatact	ggtaaaacaa	aattcttaga	ga cggtagag	aagggttaag	840
aatatattcg	tgcaggcgat	gtgatgcagg	ttgtacctgg	gcagcctatg	gtttctgatt	900
tttagtgaga	agctttacag	gtttaccgtg	cattacgtca	tttaaatcca	tcacotttate	960
tattctctgt	tcaaggacaa	acgattactg	ataaaaaacc	atttctatatt	gttgggttcat	1020
cacgggaat	tttatctcgt	ttagaaaatg	gtattgtcat	agtttcgacct	ttggcaggaa	1080
ctagaccggc	cggttaaaact	aaagaagaag	atatagcatt	agaaaaagat	gttcttctctg	1140
atgaaaaaga	gattgtcgaa	catttaatgc	tgattgatct	tggggcaaac	gatgtagggc	1200
gcgatctcaa	aaatggttag	gtccaagtta	cggatcaaat	ggtgatcgag	cgcattccac	1260
atgtcatcga	tattgtttca	aatgtacaa	gtgaagtgcg	tgatgatact	gatgcagttg	1320


```

atgtatttaa agccaccctt cggcgaggaa cgttatcagg tgcccaaaa attcgtgcaa 1380
tggaatttat tgatgaagta gagcctgtga aaagaggagt ttttgccggg gctgttggtt 1440
atttgggatg gcattggtgaa atggatatgt cgattgcaat cgtactttgt gttatccgtg 1500
acaaaaaggt gtatgtacag gctggtgcag ggctagtgtc tgactcaaat ccagaatctg 1560
agtggaatga aacccaaata aaagctcgcg cagtgatcaa agcgggttga ttatcatcaa 1620
acggattgat ttatgagtt tttagcggtt ttttaaaaa aaccgcttgc atcgtttggg 1680
agttttgcta aactgcacac cgttccgata cgaacgttac gaaacactaa gaaacgccgg 1740
catagctcag ttggtagagc aactgacttg taatcagtag gtccacagtt cgaatccgtg 1800

```

```

tgccgcgacc attttaaagt gttaagttaa tt 1832

```

```

<210> 741
<211> 382
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Acinetobacter baumannii

```

```

<400> 741
cacaaatgaca ttgcaagcaa ttgctcaatg tcaaaaaatct ggtggtaoat gtgccttcac 60
tgatctgtgag cagccctcag accctcaata tgcaacgaag cttggtgtga atattgataa 120
cctacttctgt tcacaacccg acaatggtga gcaagcactt gaaattgctg acatgcttgt 180
cogtccagcg gcaattgtat taatcgttgt ggaactcggt gctgcactta cccctaaagc 240
agaaaatcgaa ggtgagatgg gtgactctca tatgggtcta caagcgctgc ttatgagcaa 300
ggcacttcgt aaaaatcagg gtaatgctaa acgttcaaac tgtatgggtta tcttcattaa 360
ccagattcgt atgaaaattg gt 382

```

```

<210> 742
<211> 344
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Acinetobacter baumannii

```

```

<400> 742
aaatctgcgcc gtgtcgttgg tgaagtaatc ggtaaatata acccgcatrg tgaactcagc 60
gtttatgaaa ccattgttgc tatggctcaa gactttagct taacttattt attggttgat 120
ggtcagggtta acttcggttc gatcgatggc gatagcgccg cggcaatgac ttataccgaa 180
gtccgtatga ctaagctggc acatgagctt cttgcagatt tagaaaaaga cacagttgac 240
tgggaagata actacgacgg ttccggaact atccctgaag tacttccga c acgtgttcca 300
aactgtttaa tcaacggtgc tgcgggtatc gccgtaggta tggc 344

```

```

<210> 743
<211> 909
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Acinetobacter baumannii

```

```

<400> 743
gataatagct ataaagtctt aggtggctta caccggcgtg gtgtttctgt tgttaacgca 60
ctttcaagta aattgcactc aacaatttac cgtgctggct aaatccatga gcaagaatat 120
catcatgggtg atccgcaata tccattgcgt gtgattgggt aaacggata a taccggaaca 180
actgtacggtt tttagccaa gtcagaaaaa ttacgtcaaa ccatittta a tgttgaatat 240
ctagcacgcc gtttaactga gctttcttcc ttgaatgctg gtgtacgta t cgttttaact 300
gatgaacgta ttaaccttga ccatgtgtat gactatgaag gcggtttat c ttatttggg 360
aaatacatca acgaaggtaa aaacatctc aaacgaatct tccattcca c agctgatgct 420
gacaacggta ttgctgtaga agttgcattg caatggaacg atagttacc a agaaaatgtt 480

```

```

cgctgtttca caaacaacat tccacaaaa gatggtggtga cgcactttagc aggtttccgc 540
cgagcttttaa cacgttggett aaaccagtat ctggaaaaatg aaaatatctct caagaaagaa 600
aaagtgaatg tgacttggtga tgatgcgcgt gaaggttttaa cagcgattat tctgtttaag 660
gttctctgac caaaaattctc gtctcagaca aaagaaaaat tggttatcag tgagggtataa 720
ccagcggtag agcaagcaat gaacaaagag ttctctgctt acttacttga gaatccacaa 780
gctgcacaaat caattgcagg caagattatt gatgctgcac gcgcacgtga tgctgcaagt 840
aaagcacgtg aaatgacacg ccgtgaagat gcattagata ttgcaggtt tt gcctggttaa 900
ttgctgtag

```

<210> 744

<211> 1430

<212> DNA

<213> Artificial Sequence

<220>

<223> *Acinetobacter baumannii*

<400> 744

```

aacctgctct ttctgtgagt cagtaaatga cttttcttgt atatggtaga gtttaggtag 60
cgaaactctg ccattttttt tatctatggt atattttccg cagtttttga attttgacta 120
tttgaggcaa accgcttggt gacccatttt tggtaacaa cgcactttca tttattaaaa 180
ccgtttttatc gtttgccggt aaaaagacgt gcagaaagtc tagaattata tcagcaggaa 240
tgctgtgaaa gatttgggct atttgaagca ccgaagaatg taaaagcgtat ctggtttcat 300
gctgtctcag tcggggaaac caatgctgca cagcccttaa ttgaatatca cctaaaaact 360
ggcgagccag tcttagtgac caataccacg aaaaacaggtc aggcctgtgc caagtcaact 420
ttctaaaaag aaccataatt agattttatt caagccgttt atttgctctg agaccagaag 480
cctcttttaa aaaaattttt tgagttatat cagccaaagc ttttagca ct ggttgaaact 540
gaactctggc caaatttaat cgatcaagcc aaattacagc atgtacct tg tttgtgctt 600
aatgctcgtg tgcagaaaa atctgcaaaa ggatattgga aagtctcggg ttttaaccga 660
ggatatgttaa aacagctgga ctgggtgtta gctcaagata gtgcaact cg tcagcgttat 720
gttgagcttg gtttagacga acacaaaagt caggtcgttg gtaatat aa gtttgatat 780
catgcgcagc aggcgttttt taacaaagct gcccaattgc atcagcaa.tg gtatctggaa 840
aatcggcagg ttgtgacgat tgcagtaga catgcacccg aagaacaa.ca aacttttgaa 900
gcaactgcac ctatttttaa ttcatagcgt gagttggtgt gtattgtgtg gctcgtcat 960
cctgagcgtt tcgatgaagt atttgaatt tgccaaaatt taaattta at taagcatcgt 1020
agaagtatgg gccaaagtat tcatgcagc acgcaagttt atctcgtc ga cagtatgggt 1080
gagctctggt tatggtagc ottaagtcag gtgtgttttg taggcgtt tc tttaaatgag 1140
ccgggtgggg ggcataatat tttagaacct atggttttaa atgtacct ac tgtagttaga 1200
ccgcgttatt ttaactttca aacgattgtc gatgagttca ttgatgaa aa tgcgtgtcgt 1260
attgctcaag atgcgcagca ggtcgttgat atctggttag catgtctgc agaacttag 1320
gcgaactaac agtttagtat acagcgcat aaagtgttc aacgtaat ca aggttcccta 1380
caaaaacata tcggggtgat taatcgctat ctggccgaaa aatcatga at 1430

```

<210> 745

<211> 3609

<212> DNA

<213> Artificial Sequence

<220>

<223> Concatenation of *C. jejuni* genes

<220>

<221> misc_feature

<222> 478-527, 1005-1054, 1457-1506, 2014-2063, 2562-2611, 3071-3120

<223> n = A,T,C or G

<400> 745

```

atgatagggt aagatataca aagagtatta gaagctagaa aattgatttt agagatcaat 60
ttgggtggaa ctgctatttg aacaggaatt aattctcctc ctgattat cc gaaggttgta 120
gaaagaaaaa taagagaagt gacaggtttt gaataactgt tggctgagga ttaactcgag 180

```

```

gcgactcaag atacgggagc ttatgtacaa atttcaggtg tttttaaacy tgt tgcaaca 240
aaacttttcta aagtatgttaa tgactttaaga ctttttaagta gtgggtccaaa atg tgggtctt 300
aatgagattta atcttccaaa aatgcaacca ggtagttcta tcatgccagg tag ggttaaat 360
cctgttatttc ctgaagtagt taatcaagtt tgttattttg tttattggagc aga cgttaact 420
gtaaccttttg cttgtgaggg tggacaatta caacttaats tttttgaacc agt tgttannn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnngat cct tttaacgg 540
ctgatctctac tatcatagta ttttgtgatg tgtatgatat ttacaaagga caa atgtatgt 600
aaaaatgtcc aagaagcata gcaaaaaaag caatagaaca ccttaaaatag agt ggcctag 660
ctgatactgc ttacttttga ccagaaaaat aattctttgt ttttgatagt gta aaaaatag 720
ttgatactaac tcatctgtct aagtatgaag ttgataccga ttgataccga agaaacaa ggt ggtatatt 780
atagagaattt tccatgatgc taacaactgt gacacagggc aagaaacaa ggt ggtatatt 840
ttccagtttgc gccacttgat tcttttagtag atattcgttc tgaaatggtt caa acccttg 900
aaaaagtagg tctttaaact tttgttcatc atcatgaagt tgcaaaagga caa gctgaaa 960
taggagataa ttttggcaag cttgtagaag cagctgacaa tgtttnnnnn ttttnnnnnn 1020
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnngaaatg aaaaaacgtt cttttatcca 1080
tgaaggttat caccgtcttt ttgattcttt ccttgataat gctcatccta tgg cagttttt 1140
acaaggtgct gttctcatgc ttagtgcctt ttatcctgat catttaaaac tga atgtataa 1200
agaagaatat atggaaatgg cagctagaat agtagctaaa atccctacta tag tgggcaac 1260
cgcttataga tataaacacg cctttctcat gctttctcca aatttagata tgtgtttttac 1320
agaaaatttc ttatatattgt taagaaccta tcttaacgat catgtagagc tta aacctat 1380
agaagttaaa cactcttgata cagtttttat gcttcatgca gatcatgagc aaa atgcttc 1440
aactctcaaca ctttgtnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1500
nnnnnnngcg gacactttaac tcatggtgca aaagttaagt ctccgggcaa aat gttatgaa 1560
agctgttttt acggcgtaga acttgatgga agaattgatt atgaaaaagt aag agaaatt 1620
gctaaaaaag aaaaacocaa acttatagtt tgtggagcta gtcgttatgc aag agttagt 1680
gattttgcta aatttagaga aattgtgatg gaaataggtg cctatctttt tgc ttgtata 1740
gcaatattgc caggtcttgt ttgtggcaggt gacgatccaa gtccttttcc atacgctcat 1800
tgtagtaagt caactacaca taaaaactttg cgtggcccaa gagggtggtat tat ttagaca 1860
aatgatgaag agtctgttaa aaaaattaat tctgcatttt aatttaactc tca aggtggt 1920
cctttgatgc atgtaattgc tgcaaaagca gtaggattta aatttaactc tca aggtgag 1980
tgaaaagtgc atgcaaaaca agtaagaact aatnnnnnnn nnnnnnnnnn nnnnnnnnnn 2040
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aatttggga gctttacatc 2100
ctgcaaaatt agctgctgag gtaaaagcgt tgcgtgcaaga tgtggcgttt gcttttgatg 2160
gtgatgcaga tcttttgggt gttgtagatg aaaaagcgga agtggctaat ggggtagatt 2220
tattggcggt attggcaact tatcttaaag aacaaggtaa attacaatca agt gttgtggt 2280
ctactataat gagttaattg gctttaaaag agtttttaaa taaacatggt atgagcaattg 2340
atactgttaa tgttggogatt gaataatgctc ttgaaaaact ttgaaaaact gctggaatt 2400
ttggtggaga acaaaaggtg catattattt tttagcgata tgcaaaaaatc ggaagtggtt 2460
tgtagtcgct atttgcattt agtgccttaa tgcctttcaa tnnnnnnnnn nnnnnnnnnn 2520
ttttgggtca agttaaactc tatcctcagc ttttaaccaa tnnnnnnnnn nnnnnnnnnn 2580
nnnnnnnnnn nnnnnnnnnn nttacattta agcgctgatg acttaagctt 2640
agaagattctt aaaaatttcc gccaaactca tcttaaaacc cctggacacc ctgaaatttc 2700
aactcttgta gtagaaatgc ctacaggccc tttaggacaa ggcgttgcaac agt gcttaggt 2760
ctttgctatg gcaacaaa aaagcaca aa ttgttaggc atttctttaa tcatcataa 2820
aatttattgt atttgcggag atggggattt acaagaagcg atttctttaa agtctgttc 2880
tttagcagga cttcacaaac ttgataactc catacttatt tatgatagca acatatactc 2940
tatagaaggg gatgttaggt tagcctttaa cgaattgtga aaaaatggtt ttgaagcaca 3000
aggatttgaa gtttttaagt taataggaca cgattatgaa gaaatcaata aagccttaga 3060
acaagctaaa nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3120
cgcggtgctc oagatctcgc ggccttcaag tacttagctc tactatagctc tttatgatga 3180
gggtgaattt tttagacaaa cgcataacat gctttaaatt tttagacaaa tttagacaaa 3240
catgctgtag ctctatcgca aatgtctttg attttacgtc gtcctccagg tctggaagct 3300
tatccaggtg atgtttttta cttctattca agattgcttg aaagacaa caagcctaaat 3360
gatgaattag gtgctgtgtc tttagcggca ttgcgcgataa ttgaaacaa agcaggagat 3420
gtttctgctt atattccaac taatgttatt tcaattacag atggacaaat tttcttagaa 3480
actgatttat ttaactcagg aattcgtctc gcaattaatg ttggtttatc agtatctcgt 3540
gtaggtgggg ctgctcaaat taaagctaca aaacaagttt caggacatct aagacttgac 3600
cttgcctcaa 3609

```

<210> 746

<211> 1214

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> *Bordetella pertussis*

<400> 746

```

ttcgggatgg  gcatgggcgt  cgcacacgac  gtcgaaaccc  gtgcgggttt  catccagtgc  60
gggttccctg  tgcacgcgtg  ccacgcgcag  gccgaactg  cgggcgatgt  cgcgcgtcgtc  120
gggtcgcgtg  cggccatcga  gcaggcgacg  cagogaagat  ttgccgcgcg  cgttgccgcc  180
gatcaggcgc  atgcgcctgc  ctctcctgat  gccgaactgc  gcgtgggtca  gcaagggggtg  240
gtggccgtag  gccagttgaa  cgtcggtaag  cgttaataag  gaagcgaggg  ccatggacag  300
acagagtgat  gcgtattggc  ctgtattgtc  gcaggaaacg  cggggcgagg  cagcgcgcgcg  360
ccgggagccg  gggcgccgac  tgtactaaaa  tgcgcgtcgc  agggcagatc  ggccaatcgc  420
gggggatgca  aatccttcga  ggaaggctcg  gactccacag  ggcgggatag  cggctaaccg  480
cgcctcggcg  acgctggcgg  gcttgccgcg  cggaaaaagc  gaggaaacag  gccacagaga  540
cgagtctgtc  atgaggggcg  gcctggcgcg  caccggcagc  gccatctcgc  tgcgcgcgcg  600
tcgggaaacg  ggcgcggcca  tgacagggtg  aaacgcggca  acccttatcc  ggagcaaatc  660
aaaataggca  tgcgtacggc  cgttaaggcg  ggaaggcgcg  ctccgtccaa  gcattgcgggt  720
agggtgctgg  agcgttcocg  caatgggttc  ccaagaggaa  tgattgcccg  ccgggggaaac  780
ccggcgtaac  gaatccggcc  tatagatctg  ctctgcactg  cattttcatg  acagccggccc  840
ggaatccggc  agcgtgcctt  accggccctc  acgtaaaaca  atgaaagcac  gcgccacagg  900
cctaacttgc  atgaatgaca  tttaatatgc  gccgcaagct  gctgatttat  cagcaagttt  960
tcgcgcgcgc  cgtttttaca  ttggctctaa  gtctctgttg  tgattgaaaa  aatttgcaacc  1020
acgcctctga  cccatgaaag  tgcctccgcg  agagtgggaa  aaagtgaaga  ttgtgtcaac  1080
taagtggggc  aaacgggtgt  tcagggaag  cagcgcacgc  acgtttggatg  ctaaggggcg  1140
gatctcgatt  ccgacccggc  atcgtgacgc  gctcatggac  cgtgccgaag  gcccggttgac  1200
cctgaccctg  catc  1214

```

<210> 747
 <211> 925
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Burkholderia mallei*

<400> 747

```

gaccgatccg  gcaagccgcg  gcttcgcgcg  gctgcgggtg  ctgggcgtgc  ccggctgggtg  60
gccggcgaa  gcgtcgcgcg  ccttctacga  cgtatccgcg  gtgtttcgcc  cgggcccgcg  120
acgcgacacg  gatgtctctg  ccgctgcgcg  gtgacggagc  acgcttgctc  cgcgcgcgcc  180
gcgcgcgcgc  gcgcaccgcc  ggtgcgcgct  ttgcgcgaag  ccgcgcgcgc  ggcaaggggcg  240
tcgcgcgcag  cggatgcgcg  tgtacgggtg  tagaatcccg  ctgcgaaggc  aggttaggca  300
ctgcgcggct  tcgcgggttc  ccgcgaaggg  cggaggaaag  ccggactcca  acaggcgagg  360
gtgatggcta  acggccatcc  gtggcgacac  gccgaacagg  gcaaacagaa  gcaaacccgc  420
gatggccggc  cgcgaagccg  gatcaggcaa  gggtagaaag  gtgcggtaag  agcgcaccgc  480
ggctgcggcg  acgcagacgc  gcaaggtaac  ctccaccgcg  agcaattcca  agtagggcga  540
cgcgcgatct  cggatgcagg  accgtgcgcc  cgtctcgttc  cggggttaga  agcttgagcg  600
cgtgcgaat  ggcgcgccta  gaggaaatgc  ttgcacggcg  cgcgcgcctt  cggcgctgag  660
gttgacacag  aatccggctt  atcggccgcg  ttgcgcgcgc  gatgacgaaa  ggccgcggcc  720
cgatgcggcg  ccggcccttt  ttccgtttcg  cggtcgcgcg  gcacggcgcg  ttgacgggac  780
aagcgcgcta  ccgcgcgacg  atttcgaacg  aatgcgacag  ctgcgcgctc  ttgcgcgata  840
tgatcgacgc  cgaaacgat  ttgtcgtgcg  acagattgat  cgcgcgcctc  accggtcgcg  900
ggttcagggt  gcggcccgct  accgt  925

```

<210> 748
 <211> 713
 <212> DNA
 <213> Artificial Sequence

<220>

<223> *Bacillus subtilis*

<400> 748

```

gttcttaaacg ttcggggaat cgtgcagat cttgaatctg tagaggaaa g tccatgctcg 60
cacggctgctg agatgcccgt agtgttcgtg cctagcgaa g tcaataagct a gggcagctct 120
tagaggctcga cggcaggaaa aaagcctacg tcttcggata tggctgagt a tccctgaaag 180
tgccacagtg acgaagtctc actagaaatg gtgagagtgg aacgcggta a acccctcgag 240
cgagaaaccc aaattttggg aggggaacct tcttaacgga attcaacgg a gagaaggaca 300
gaatgctttc tgtatagata tgattggcgc ctgagtaaga ggtgatgag c cgtttgcagt 360
acgatggaa c aaacatggc ttacagaacg tttagccact tacatttaa a atgtagaaaa 420
caagctctcc cgtataaagg gagcttttat cttgaaaaga gaaaagttt t aaaagacagg 480
gtgatacagat gaagaagtat acactaattg caacggcgcc gatggcgat t gaagctgttg 540
tcgcaaaagg agtacagagat tttagatacg aatgcaaggt tgataacgg c aaagttattt 600
ttgaagggtg tgcaattgcc atctgcgcgt gaaacctttg gcttagaac a ccgacgcga 660
taagggttca ggttgtctct tttaaaggca aaacatttga tgaactgttt gaa 713

```

<210> 749

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<223> *Clostridium perfringens*

<400> 749

```

aaaacaagtt ctttttcata taatgatgta taagtaatac ttagggtggg gaattatgtg 60
gtccaatttt ggaatatagat ttaatggaga ctgctttaaa gacttaaggg gagatttcaa 120
tagattaatg agaaatttta agagaaatgc ttgtaaaaga tgtcttattc ataattgcta 180
tttcagaaat gccctaaagt ggggggctgt aggtggcata ttaaccttcc ttataataag 240
tcaaataggga gttccttttag caattgtttg tattgggaata gtacgaata t ttgtgatttg 300
taataaatgg tagaaaaaat aatttgaaaa aaataagtat atatgttaa t attaatottg 360
cgagtaagcc agacaatcgc tgcagtctct agaaactagg gaggaaagt c cgagctccat 420
agggcaggat gctggataac gtccagtggg ggtgactcta aggtagtgc a aacagaata 480
aacgcgctag atttatctag gtaagggtgg aaaggtgagg taagagctca ccagggtata 540
ggtgactata ctgctatgta aaccccatct ggagcaagac caaataggag gacatatagg 600

```

```

gggtgcocgt cccgtccctg ggtgtgtcgc ttgagccctat cggcaacgggt aggcctagat 660
agatgattgt caaatacaga actcggctta tagacttata tcgtatttta aaaaacagt 720
gttataatca ctaagtgttt tttattttta caaaaaata tactgtagat t tctttccct 780
attaacttta atcttacagt attaatttta ttttattgga tatactca 828

```

<210> 750

<211> 777

<212> DNA

<213> Artificial Sequence

<220>

<223> *Escherichia coli*

<400> 750

```

gaagctgacc agacagtgcc cgttcgtcgc tcgtctctt cggggggagac gggcgagggg 60
gaggaagtc cgggtcccat agggcagggt gccaggtaac gccagggtg gaaacccacg 120
accagtgcaa cagagagcaa accgccgatg gccgcgcaa cggggatcac gtaagggtga 180
aagggtgcgg taagagcgca ccgcgcggt ggttaacagtc cgtggcacgc taaactccac 240
ccggagcaag gcgcaaatagg ggttcataag gtacggcccg tactgaaccc gggtagggctg 300
cttgagccag tgcagcattg ctggccctaga tgaatgactg tccacgacag aaccggctct 360
atcgtctcag ttcaactgat ttacgtaaaa acccgcttcc gcggtttttt gcttttggag 420
gggcagaaa agtaatgaat gtccacgacg ctatacccaa aagaagcgcg cttatcggtc 480
agtttccact ggtttacgta aaaaccgcgt tcggcggttt ttgtctttt gaggggcaga 540
aagatgaatg actgtccacg acactatacc caaaagaag cggcttatcg gtcagtttca 600
cctgttttac gttaaaaacc gcttcggcgc gtttttactt ttggaggtca 660

```

atgactgtcc acgacactat acccaaaaaa aagcgggtta tcggctcagtt tta<ctgatg 720
 tacgtaataa accgttccgg cgggtttcag attgttgagt gcgctttatt cat<gcgcg 777

<210> 751

<211> 834

<212> DNA

<213> Artificial Sequence

<220>

<223> Rickettsia prowazekii

<400> 751

taataaatta atttattcat atcaaaagttt gctaatagtg tatatgtttt taagtactac 60
 attatttata cattaggaaa aaaatagtag caatgtttaa ttaagatato ttt<ctttaa 120
 gaattgacat tatggaattt gttattataa ttgttaattat attgtgtgta caat<aattac 180
 aataaatttt cccctcagaa cctaacaagc taattgaaat tcttttaaca tat<tattgac 240
 taatttaazga aaagctacca taatctaaat ggtcgtgcag ttgcgtgatg ata<atcagca 300
 ggaaagtccg gactctatag aggtatgggt cgggttaaca tccggcagag tat<tattact 360
 ttagggctag taccacagaa aatataccgc cgagtatttc ggtaagggtg aaa<aggtgtg 420
 gtaagagcac accggttaagt tggcaacaag ttacgcattgg ttaacccac caa<agcgaag 480
 atcaaatagg cattacagaa tttaaatatt tatttaagtt cctgggttac ct<at<atcgcg 540
 attgtaatgc gggtagatgc cttgaggtaa acggttaacgt ttat<ctaga taa<taactg 600
 caatgaatta atattcatac aga<atccgcg ttatagacca gatgagcagg tat<tacatgt 660
 gttaatccgc cagagttatt gcgagtaact gaaaaaagta tggcaatcta gaa<aataat 720
 cagattctgt gga<tttttag tgttc<ctgcg caatga<gaa aataat<acac gtatagatta 780
 cagctagga tgatactaat acttactgta acataattta atgaaaaagt t<ata 834

<210> 752

<211> 783

<212> DNA

<213> Artificial Sequence

<220>

<223> Staphylococcus aureus

<400> 752

tgatattttg ggtaatcgct atattatata gaggaaagtc catgctcaca cagt<ctgaga 60
 tgattgtagt gtt<gtgctt gatgaacaa taa<atcaagg cat<taatttg acg<gcaatga 120
 aatat<ctaa gt<ct<ctgat atggatagag taatttga<aa gtg<ccacagt g<cgtagctt 180
 ttataga<aat at<aaa<gggt gaac<gcggta aa<cc<ctcga gtgagcaatc caa<ttt<gtt 240
 aggagca<tt gtt<ta<cgga att<ca<cgta taa<cgagac ac<ctt<cgcg aa<tgga<gtg 300
 gtgtaga<ag atg<gt<atca c<gtgagtacc agt<tgacta gtgca<gtga tgag<acgat 360
 ggaacaga<ac atg<g<cttata gaa<at<cac tactag<ttta g<ct<ctcag atga<tgaga 420
 g<ct<ttttta tga<aa<gaac act<taaaatt aa<ac<ctt<gt cttgatataa tga<actg<cc 480
 ttgt<ttttaa atag<ta<gcg gat<gc<gttaa t<gtat<acgc att<aa<ttg ttg<gaa<gtg 540
 at<aaa<acaa ca<g<ctaa ga<aa<at<acc t<gtata<aaag gaga<at<ata tat<gt<tt<caa 600
 tt<ctt<g<ag ttt<g<ccgat gggattagaa g<ct<gt<gtt ctag<gggaa< t<ca<ga<atta 660
 gg<ctat<gaaa caa<at<gtga aa<at<gt<gt at<att<tttt aag<gagacgc aag<tg<ca<tt 720
 gta<aa<gg<caa att<at<ggtt gcgca<agca gac<ga<atca aa<att<gtt<gt tgg<g<ctttt 780
 aac 783

<210> 753

<211> 1086

<212> DNA

<213> Artificial Sequence

<220>

<223> Vibrio cholerae

<400> 753

```

gtgaaatcgg  tctggcgatc  gagatgggct  gtgatgcaga  agacatcgca  ctgaccatto  60
atgctcacc  aacgctgcat  gagtctgtgt  gctctggcgc  tgaagtattc  gaaggcacca  120
tcactgacct  gccaaacgcc  aaagcgaaaa  agaaaaagta  attctgattc  cactggtttg  180
gttaaaaagt  gtttgattga  agaaccgcct  gcttgcaacg  gtttttttcc  gcttttgatt  240
cccaattgaa  tgcaaaagta  gcagttaaac  cgagatttaa  cgcgctggcg  gattgtttct  300
ggactctgt  caccattctc  gctacaatcc  gcgcgggagt  tgactgggtg  agctgctgct  360
tattgacgtc  ccttgcccta  tgcgccagga  gactgataag  ggggaggaaa  gtcggggctc  420
catagagcag  ggtgccaggt  aacgcctggg  gggcgcaagc  ctacgacaa  tgcaacagag  480
agcaaacgc  cgtggccctc  tccttcggga  tgggatcagg  taagggtgaa  aggggtgcgt  540
aagagcgac  cgtgcgactg  gcaacagttc  gtacgagggt  aaactccacc  cgggcaagaa  600
ccaaataggc  ctccacatag  cgttctgcgc  gttaggaggc  gggtaggttg  cttgagccag  660
tgagtgaatt  ctggcctaga  ggaatggcta  ctaccgcgca  agcggaaacg  aacccggctt  720
atacgtcag  tccacctatt  gcagaccatt  catagccctg  tgttatggct  ggttttttgc  780
tttttgcga  ctcaagtaac  agcaaaacca  ttaaacctag  ccgaagtcca  gctcctgtat  840
acgottatg  ctacgggtag  tgtctgaat  cgggtacacta  acccatatga  cgggcatgcc  900
cagcacaac  agaaaaatct  gactgctctc  ttccaaacaa  tctctgtatt  attgaaacga  960
tcgattgaag  gattggcgat  caagccggat  ggttatctca  tcgatggcac  ctttggccgc  1020
ggtggtcaac  gtgcaccatt  tctcgctcag  ttaggccacg  aaggtcgtct  gtacagcatt  1080
gacggt

```

<210> 754

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> *Coxiella burnetii*

<400> 754

```

gagttaacg  gagtatccat  cgtgacttac  caacacatca  aagttcccaa  ccaaggtgaa  60
aaaaatcac  ttaataaagc  cgttttagaa  gttctcgacc  gaccatttat  tccctttatc  120
gaaggagatg  gattggcat  tgatatcgcg  ccgctaatga  aaaaactggt  cgtatgcgcc  180
gtggaaaaat  cctacgctgg  aaagcgaaaa  attgaatgga  tggagatcta  cgcgggagaa  240
aaggctacga  aattgtatgg  caaagacaat  tggctgcctg  atgagacata  cgaagccatt  300
aaagaatacc  aagtggccat  taaaggtccc  ttaaccacgc  cgggtggggg  tggcatacgt  360
tcgctcaat

```

<210> 755

<211> 1317

<212> DNA

<213> Artificial Sequence

<220>

<223> *Acinetobacter baumannii*

<400> 755

```

attacgacg  aaattgtaag  taattttgtc  aataattttc  ttgattaama  ttatcaagca  60
cttggaaagt  ctatcaagtg  tttgtatgat  tcaaatgtga  atagcttaaa  aataatactg  120
gggttaaaaa  atatctcagg  ggccaataaa  tttaggctga  gcttgaaaca  caattgttat  180
ctctggagg  tatccatgaa  attgagtcgt  attgcaactg  ctactatgct  ttgtgctgct  240
ccattgacgt  ctgctaatgc  tggcgttaaa  gttactccat  tattgcttgg  ttacacttcc  300
caagagacgc  aacacaacaa  tggcggtaaa  gatggtaact  taactaacgg  tctcgagtta  360
caagacgatt  tattcgttgg  cgcagctctt  ggtatcgagt  taactccatg  gttaggtttc  420
gaagctgaat  ataaccaagt  taaaggcgac  gttagcggcg  ctctctctgg  ttctgaatat  480
aaacaaaaac  aaatcaacgg  taactcttat  gttactttct  atttaattac  taaaaactaa  540
gacagcaaaa  tcaagccgta  cgtattatta  ggtgctggct  gctataaatc  cgaactttga  600
ggcgtaaacc  gtggtacacg  tggtaacttt  gaagaaggta  ctttaggtta  cgtggtgtgt  660
ggtgtcttt  ggcgcttaaa  cgaagcttta  tctctctgta  gctgaagctg  tgcactattt  720
aatgctgatg  aagagttctg  gaactataca  gctcttctgt  gcttaaacgt  atgtcttggt  780
ggtccattga  agcctgctgc  tctcttagta  gaagttgtcc  cagttgaacc  aaccacgatt  840
gctcaccaac  caaagagatt  aactgaagac  ctlaacattg  aactcgtgt  gttctttgat  900

```

actaacaat	caaacaatcaa	agaccaat	aagccagaaa	ttgctaaagt	tgtcgaaaaa	960
ttatctgaat	acccataacg	tactgcaagt	atcgaaagtc	acacagataa	caactgggtcca	1020
cgtaaggtga	acgaacgttt	atcttttagct	cggtctaact	ctgttaaatc	agctcttgtga	1080
aacgaataca	acgtgtgatgc	ttctcgtttg	tctactcaag	gtttcgcttg	ggatcaaccg	1140
attgtgcaga	acaaaaactaa	agaaggtcgt	gctatgaacc	gtcgtgtatt	cgcgacaatc	1200
actgtgtacc	gtactgttagt	agttcaacct	ggtcaagaag	cggcagctcc	tgccagcagct	1260
caataatttg	agttctttgaa	cagtaaaaaa	gcgactcggt	agagtcgctt	ttttatag	1317

<210> 756

<211> 4932

<212> DNA

<213> Artificial Sequence

<220>

<223> Rickettsia prowazekii

<400> 756

atggctcaaa	aacccaattt	totaaaaaaa	ataatttcog	caggattggg	aaactgcttcc	60
acggctacta	tagtagctgg	ttctctctgg	gtagcaatgg	gtgctgctat	gcaataataat	120
aggacaacaa	atgcaagcgc	tacaaccttt	gatggtagat	gctttgatca	agctctgtgt	180
gctaattatc	ctgtgcgtcc	aaattcagtt	attactgcta	atgctaatca	tctctattact	240
tttaattact	caaaagctga	tttaaatagt	ttatttttgg	atactgocaa	tgaatttagca	300
gtaacaatta	atgaggatgc	tacotttaga	ttatatacaa	ataattgcta	gcaggctaaag	360
ttottttaatt	ttactgttgc	tgctggtaaa	attotttaaca	taacagggca	gggtatttact	420
gttcaagaag	cttctcaatc	aataaatgct	caaaatgctc	ttacaaaagt	gcactgggtgc	480
gctgctatta	acgctaatga	totttagcggg	ctaggatcaa	taacctttgc	tgtcgccgct	540
tctgtattag	aattttaattt	aataaatctc	acaactcaag	aagctcctct	tacacttggg	600
gctaatttcta	aaatagttaa	tggtggtaat	gggacattaa	atattactaa	tggtatttat	660
caggtttcaa	ataaacacttt	tgctgggtatt	aagaccattaa	atatcgatga	ttgtcaaggt	720
ttaatgttcta	attctactct	tgatgcgcgt	aatacttttaa	atttacaagt	aggttggtaat	780
actaatttaatt	ttaatggaat	agacggtact	ggtaaattag	tatttagtcag	taagaatggt	840
gctgcctacc	aatttaattgt	tacaggaact	ttaggtggta	atctaaaagg	tattattgaa	900
ttgaacaact	cagcagtagc	tggtaaaoct	atctctcaag	gagggtgctc	taattgcagta	960
ataggtacaag	ataatggagc	aggtagagct	gcaggattta	ttgttagtgt	tgataatggt	1020
aatgcagcaa	caatttctgg	acaagtttat	gctaaaaaca	tggtgtatca	aagtgcctaat	1080
gcagggtgac	aagtaoottt	tgaacacata	gttgatgttg	gttttagcgg	tacacaccaa	1140
tttaaaaact	cagatttcta	agttataata	acagaaaact	caaacctttg	ttctactaat	1200
tttggtaatc	ttgacacaca	gatttgtagc	octgatacta	agattctctaa	aggttaacttc	1260
atagggtgat	taaaaaataa	cggtaatact	gcagggtgtga	ttactttttaa	tgctaatggt	1320
gcttttagtaa	gtctgatgat	tgatccaaat	attgcagtaa	caaatattaa	tgcaattgaa	1380
gcagaagagg	ccgggtgtgt	agaattatca	ggaatacata	ttgcagaatt	acgttttagtg	1440
aatgtgtgct	ctatctttaa	acttgtgat	ggcaacagtaa	ttaatggctc	aggttaaccaa	1500
aatgtctcta	tgaataataa	tgctcttgca	gctgggtcta	ttcagtttag	tgggagtgct	1560
ataattaccg	gtgatattag	taacgggtgt	gttaatgctg	cggttacaaca	cattacttta	1620
gctaaoagtg	cttcaaaaat	attagcactc	gatggcgcaa	atattatogg	ggctaatggt	1680
gggtgtgcaa	ttcattttca	agctaacggt	ggtaacttta	aattacaaca	tactcaaaat	1740
aattattgtg	ttaattttga	tttagatata	actactgata	aaacagggtg	tggtgatgca	1800
agtagttttaa	caaatataat	aactttaact	attaatggta	tcttcggtag	tggtgtagct	1860
aatactaaaa	caacttgaca	atlaaacatc	gggtcaagta	aaacaaatatt	aaatgctgct	1920
gtgtgctgta	ttaacagagt	agtttatagaa	aaaaatgggt	cagtaacaact	taactcaaat	1980
acttaotttaa	taacaaaaac	tatcaatgct	gcaaaacaa	gtcaaaataat	oggtgcoctg	2040

gatcctctta	atactaatac	taoctttgct	gatggtacaa	atttaggtag	tgcaaaaaat	2100
ccactcttcta	ctacttaatt	tgccactaaa	gctgctaagt	ctgactctat	atttaaatgta	2160
ggtaaaaggag	taaattttata	tgctataaat	attaactacta	acgatgctaa	tgtaggttct	2220
ttcaactttta	gggtctgtgg	tacaagtata	gtaagtggta	cagttgggtg	acaggcaagg	2280
cataagctta	ataattttaat	attagataat	gtgactactg	ttaagttttt	aggtgataca	2340
acattttaatg	gtgggtactaa	aattgaaggt	aaatccatct	tgcaaaatag	caataaattat	2400
actactgac	tggttgtaac	tgctgataat	actggtaaat	tagaattttg	taactcagct	2460
octataacgc	taacattaaa	taaaacaggt	gcttattttg	gtgtttttaa	acaagtaatt	2520
atttctgtgc	caggttaacat	agtattttaat	gagataggta	atgtaggagt	tgtaacaggt	2580


```

atagcagcta attcaatttc ttttgaatt goaagtttag gtacatottt att ottacot 2640
agtgttactc cattagatgt ttttaacaatt aaaagtacog taggtaatgg tac agtagat 2700
aatttttaag tctcatttgg agttgtatca ggtattgata gtagatcaaa taa cgggtcaa 2760
atcatoggtg ataaaaagaa tatttatagct ctatogcttg gaagtgtataa cag tattact 2820
gttaatgcta atacattata ttcagggtatc agaactacaa aaaaataatc agg taotgtg 2880
acacttagtg gtgttatgoc taataatcct ggtacaattt atggtttagg ttt agagaat 2940
ggtagtccaa agttaaaaca agtgacattt actacagatt ataacaaott aggt tagtatt 3000
attgcaataa atgtaaacaat taatgattat gtaactctta ctacaggagg tat agcaggg 3060
acagattttg acgttaaaat tactcttgga agtgttaacg gtaacgctaa cgt aaagttt 3120
gttgatagta catctttctga toctagaagt atgattgttg ctactcaagg taa taagggt 3180
actgtacttt atttagttaa tgcattagtt agtaatatcg gtagtttaga tac tctgtta 3240
gctctcgaac gattttacag taatgatagt ggggcaggat tacaaggcaa tat ttattca 3300
caaaatatag atttttgctg ttataattta acatttctaa attcotaagt cat tttagggt 3360
ggtaggtacta ctgctattaa tgggtgaaatc gatottctga caaataattt aat atttga 3420
aatggtactt caacatgggg tgataatact tctattagta caaogttaa tgt atcaagc 3480
ggtaatatag gtcaagtagt cattgcccga gatgtccaag ttaacgcaac aac tacagga 3540
actacaacca ttaaaaatca agataatgct aatgcaaat tcaagtggcac aca agcttat 3600
actttaattc aaggtggtgc tagatttaat ggtacttttag gagctcctaa ctt tgtgtga 3660
acaggaaagta atattttcgt aaaaatagaa ctaactacgt attctaacca gga ttatgta 3720
ttaacacgta ctacogtagt attaaacgta gttacaacag ctgttggaata tag tgaatt 3780
gcaaatgca cttggttaag toagaacatt tctagatgct tagaatcaac aaa tacagca 3840
gcttataata atatgctttt agctaaagat ccttctgatg ttgcaacatt tgt aggagct 3900
attgctcacg atacagtgct ggcgttaact acagtaact taaatgatac aca aaaaact 3960

```

```

caagatctac ttagtaatag gctagtgaca cttagatata taagtaatgc tga aacttct 4020
gatgttgctg gatctgcaac aggtgcagtg tcttcagggt atgaagcggg agt actttat 4080
gggtgatagg ctaaaacttt ctataacatt gcagaacaag acaaaaaagg tgg tatagct 4140
gggtataaag caaaaactac gttgggttga gttgggttag atactctgc tgg cgataac 4200
ctaagtattg gggcagctat tgggatoact aaaactgata taaaacacca aga ttataag 4260
caaggtgata aaaaactgat taatggttta tcaattctct tatatggct oca acagctt 4320
gttaagaatt tctttgtcca aggttaatgca atctttacot taaaacaagt caa aagtaaa 4380
agtcagcggt actcttctga gtctaattgt aagatgagca agcaaaattg tgc tggtaat 4440
tagcataaca tgacatttgg tggtaattta atatttggtt atgattataa tgc aatgcca 4500
aatgtattag taaotccaat ggcaggactt agctacttaa aatottctaa tga aaattat 4560
aaagaaacog gtacaacagt tgcataaag cgatttaata gcaaattttag tga tagagtc 4620
gatttaatag taggggtcaa agtagctggt agtactgtga atataactga tat tgtgata 4680
tatccggaaa ttcaattctt tgtggtgcac aaagttaagt gtaaatctga taa tctcag 4740
tctatgttag atggacaac ttgtccattt atcagtcaac ctgatagaac tgc taaaacg 4800
tcttaataa taggcttaag tgcaaacata aaactcgatg ctaagatgga tga tggtagc 4860
ggttatgatt ttaattctgc aagtaaatat actgcacatc aaggctactt aaa agtactg 4920
gtaaacctct aa 4932

```

<210> 757

<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> Rickettsia prowazekii

<400> 757

```

atgactaatg gcaataataa taacttagaa tttgcagaat taaaaattag aggtaaacta 60
tttaaggttac ctataacttaa agcaagtatc ggtaaaagatg taatcgatat aagtagggta 120
tctgcggaag ccgattactt tacttatgat ccgggtttta tcttactgc ttctgtcaa 180
tctactatca catatataga oggtgataaa ggcattattat ggtatcagg ata tgatatt 240
aaagactatg ctgagaaagg tgalltttta gaagtggcat atttgatgat tttggggag 300
ctaccaagta gtgatcagta ttgtaatttt actaaaaagg ttgctcatca ttcatttagtg 360
aatgaaagat taactatttt atttcaaac ttgttgagtt ctctcatcac tatgtgatatt 420
atgcttgcaog ctgtttgttc tctttcagca ttctatactg atttattaa ttttaatgaa 480
acagactatg aacttacogc tatttagaat attgtaaga taactactat cgc tgcgaat 540

```

```

tcttataaat attctatag gcaacggttt atttatctcg ataattcatt agattttacc 600
gaaaattttc tacatatgat gtttgcaact cttgttacta aatataaagt aaatccaata 660
ataaaaaatg ctcttaataa gatatttato ttacatgcag aocatgagca gaattgcttc 720
acttcaacag ttoggattgc tgggtcatca ggagctaact cttttgcagt tattagcaat 780
ggatttgcac cactttgggg gctgtctcac ggoggggcta atgaagcagt gataaataag 840
cttaaaagaaa ttggcagttc tgagaatatt cctaaatgat tagctaaagc taagaataag 900
aatgatccat ttaggtttaat ggggttttgg cctcgagtat ataaaagcta tgaccgcggt 960
gcgcagtagc ttaagaagaa ttgtaaagaa gtattaaatg aattagggtca gtttagacaat 1020
aatccgtgtt tacaataagc aatagaactt gaagctctcg ctcttaagaa tgaatatttt 1080
attgaaagaa aatttatatcc aaatgttgat ttttattcag gcatattcta taaggctatg 1140
gggtataccgt cgcgaatgtt cactgtactt ttgcaatag caagaaccgt aggttggatg 1200
gcacaatgga aagaatgca cgaagatcct gaacaaaaa ctagtagacc tagacagctt 1260
tacactgggt atgtacatag agagtataag tgtattgtag aaagaaagt a 1311

```

<210> 758

<211> 882

<212> DNA

<213> Artificial Sequence

<220>

<223> *Vibrio cholerae*

<400> 758

```

atgttcggat taggacacaa ctcaaaagag atatcgatga gtcatatttg tactaaattc 60
attcttgcgt aaaaattttc ctttgatccc cttaagcaata ctctgattga caaagaagat 120
agtgaagaga tcatcgattc aggcagcaac gaaagccgaa ttctttggct gctggcccaa 180
cgtccaaacg aggtgatttc togcgaatgat ttgcatgact ttgtttggcg agagcaaggt 240
tttgaagtcg atgattccag cttaaccocaa gccatttcga ctctgcgcga aatgtctcaa 300
gattgcacaa agtccoccaa atacgtcaaa acggttccga aacgcgggtta ccaattgata 360
gcccgattgg aaacggttga agaagagatg gctgcgaaa gcgaagctgc tcatgacatc 420
tctcagccag aatctgtcaa tgaatacgca gactcaagca gtgtgccttc ctacagccat 480
gtagtgaaca caccgcagcc agccaatgtt gtgacgaata aatcggtccc aaactttggg 540
aatcgactgc ttattctgat agcgggtotta ctccocctcg cagtattact gctcaataac 600
cogagccaaa ccagctttaa accocctaag gtgtgcgatg gcgtagccgt caatatgccg 660
aataaccacc ctgatctttc aaactgggta ccgtcaalog aactgtgcgt taaaaaatat 720
aatgaaaagc atactgttgg gctcaagcog atagaagtca ttgccaaagt tggcaaaat 780
aaccagttaa cgtcgaatta cattcacagc cctgaagttt caggggaaaa cataacctta 840
cgaatcgttg ctaaccoccaa cgatgccatc aaagtgtgtg ag 882

```

<210> 759

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> *Francisella tularensis*

<400> 759

```

atgcctaaag ttggttttat tgggtggcgc ggaatggtcg gtcagtttt aatgtctcgt 60
atgcctgaat caaaagattt tgattgtatt ttgccaaagt tttttgcac atctcaggtta 120
ggcagctgct caacaggttt tatgcaacaa tatggagogt tacaagatgc ctatagttatc 180
gaccaactaa tagtatgga tatacttcta agttgccaa gttgtgaata tcccaagaa 240
ataccacaca aattaagaga agccggtcgg caaggtttct ggatagacg tgcatcgaca 300
ctacgcttag acaagatag tactctagtt ctagaccctc taactacaga tcaaatattt 360
aatgtctatt ataattgtaa aaagatttt atcggtagta attgtactgt tagtctaatg 420
tcaatagcta tagctggact actcaagaa gatcttgtt aatgggttaa ctctagttac 480
tatcaagcaa tticaggagc ggttgccgca gcaatgcaag aactacttca ccaaaccaag 540
cttttaagca aaattgata tagagatgaa gatattctaa tttagagaaa aatcttcaga 600
gaattatcaa aagactcctc aaaaatccct caacaaaaa ctgtacaac ttgtgcttat 660
aatctattac ctctgtaga tgttggtag cctagtggac aaacaaaga agagatacaa 720

```

gcagctacag	aacttaataa	aattctagat	actaaaaaaa	caatccctgt	cgatggtata	780
tgtgtcagag	taccagatct	aagatcacac	tctcaagcat	taacagtgta	acttagacag	840
aaattaacaa	ttgaagaat	taagcaaaaa	atatctcaag	gtaatgaatg	ggttaaagta	900
atagataata	acaaagaaga	tactttaaaa	taoctaacac	ctcaagctaa	ttcaggaact	960
cttgatattg	ctataggctg	tatcaaatca	togttattag	ctgatgatat	atttcattgt	1020
ttccagtagt	gtgatccagct	attatgggga	gctgctgagc	cccttagaag	agttttaaat	1080
attattaaaa	tataa					1095

<210> 760

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> *Francisella tularensis*

<400> 760

atgaataaaa	aaatcttagt	aacaggtggt	gtaggctata	taggtagtca	tacagtggtta	60
gaactctctg	atagagatta	tcaagttgtg	gtggtagata	atctttcaaa	tagcaaaagta	120
ctctgtaaatg	acagggtgtta	aaaaatcaca	aataaagatt	ttgattttta	tcagctagac	180
cttttaggta	aagctaagct	aacaaaagtt	tttcaagagt	atgatattta	tgtgttaatt	240
cattttgctg	gctttaaagc	tgtaggtgag	agtgttgaaa	aaccgttaga	gtattatcat	300
aacaatatcc	aaggtacact	aaacttaact	gagctaattg	aagagtataa	agtttataat	360
tttgttctta	gttcatcggc	gactgtatat	gggatgaata	ataaaccacc	ctttacagaa	420
gatatgcttc	taagtacaaac	taaccataac	gggtgcaacta	agctaattgtt	agaagacatt	480
tggcgagatt	tgcaaaatgc	taataataat	tttaattatta	catgtcttag	atattttaatt	540
ccagtcggcg	cccatagtag	tgggatgata	ggagaggatc	cacagggtat	acctataaac	600
ctcatgctct	atgtcgcgca	agtaggtgct	ggtaaaactag	ctaaacttag	tacttttgtt	660
gggtactatg	agactataga	tgttacagga	gtgagagact	atatacatgt	tgtagattta	720
gcaatagctg	atataattagc	gttagaaaaa	ttatcacaaag	ataagcctag	ctggagagct	780
tataactcttg	gtctctgaaa	tggctattct	gtattagaga	ttgtcaaaag	ttatcaaaaa	840
gocctaggtta	aagagattcc	atatcagata	gtagctagga	gagccggtga	tattgacgag	900
agttttgctg	atgttgcocaa	ggctaaaaag	gagttggggt	ttgagacaca	aaagacata	960
gatgatattt	gtgatgatat	gcttaaatgg	caaaagtagc	caaaagagaa	taatatotag	1020

<210> 761

<211> 840

<212> DNA

<213> Artificial Sequence

<220>

<223> *Shigella flexneri*

<400> 761

cgccccctgg	ctgatgcogt	gacagcatgg	ttccccgaaa	acaaacaatc	tgatgtatca	60
cagatattgc	atgcttttga	acatgaagag	caagccaaaca	ccctttccgc	gttcccttag	120
cgcccttccg	ataccgtctc	tgccagcaat	acctccggat	tcogtgaaca	ggtccgtgca	180
tggctggaaa	aacctcagtc	ctctcgggag	cttcgacagc	agtctttcgc	tgttctgctc	240
gtgcgaactg	agagctgtga	ggaccgtgtc	gogctcacat	gggaacaatc	ccggaaaaac	300
ctctcgtctc	atcaggcaatc	agaaggccct	ttcgataatg	ataccggcgc	tctgctctcc	360
ctggcgaggg	aaatgttccg	cctcgaaatt	ctggaggaca	ttgcccgga	taaagtcaag	420
acctctccatt	ttgtggatga	gatagaagtc	taoctggcct	tcacagacct	gctcgcagag	480
aaaactcaagc	tctccaotgc	ogtgaaggaa	atgcgtttct	atggcgtgtc	gggaagtaca	540
gcaaatgacc	tcogcaotgc	cgaaagccat	gtcagaagcc	gtgaagagaa	tgaatttaag	600
gactgtgtct	ccctctgggg	acatggcat	gctgtactga	agcgtacgga	agctgaccgc	660
tggcgcgagg	cagaagagca	gaaatatgag	atgctggaga	atgagatacc	ctcagagggg	720

gctgacggcg	tgaagacatc	aggtctgagc	ggtgatgcgg	atgcggagag	ggaagccggt	780
gcacagggtg	tgogtgagac	tgaacagcag	atttaccgtc	agctgactga	cgagggtact	840

<210> 762
 <211> 503
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Campylobacter jejuni*

<400> 762
 aaaaacttta aaaaagctgt tttttacttg atattgtttt ttaaataatgc taaaattagg 60
 cgtttcaatt aaacaaagag agcttttatg actaaagcag atttcatttc attagtgtgt 120
 caaacagctg ggcatacaaaa aaaagacgct actactgcta ctgatgcagt tattttctact 180
 attactgatg ttttagcttaa aggtgatagc atcagtttta ttggtttttg tactttttca 240
 actcaagaaa gagctgctag agaagctaga gtaccaagca caggaaaaac aatcaaatgt 300
 cctgtctaaa gagttgcaaa atttaagcta ggtaaaaacc ttaaagaagc tgttgcaaaa 360
 gcaagcgcca aaaagaaaaa ataaaacttc ggctagataa attctagcct tttttcttaa 420
 ttaattcaga tttttgtat cttttatatta cttttatttt ttaaactttt ataaaactat 480
 cattattaaa caaaaaagga tat 503

<210> 763
 <211> 2118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Concatenation of *A. baumannii* genes

<220>
 <221> misc_feature
 <222> 447-486, 778-817, 1162-1201, 1495-1534, 1928-1967, 2115-2118
 <223> n = A,T,C or G

<400> 763
 cgcgcggttaa aactaaagaa gaagatatag cattagaaaa agattttgctg tctgatgaaa 60
 aagagattgc tgaacattta atgctgattg atcttggggc aaacgatgta gggcggtgat 120
 cgaaaaatagg taaagtccaa gtcacggatc aaatggtgat cgaacgcttat tcacatgtca 180
 tgcattattgt ttcaaatgta caaggtgaag tgcgtgatga tatcgatgca ctgatgtat 240
 ttaaagccac ctttccagca ggaacgttat caggtgcccc aaaaattcgt gcaatggaaa 300
 ttattgatga agtagaacct gtgaaaaggg gagtttttgg cggggcgctgt ggttatttgg 360
 gatggcatgg tgaatggat atgtcgattg caatccgtac ttgtgttatc cgtgataaaa 420
 aggtgtattgt acaggctggt gcaagggnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
 nnnnnnggaa ctctggcggtt tagtttcaaga tgaactcatt atcgggttag taaaagaacg 540
 tattgtctaa cctgactcgc tgaatggttg tattttcgac ggcttccacc gcaactattc 600
 tcaagcagaa ctttgggaaa aagaagggat cagcattgat catgtaattg aaattgatgt 660
 acctgatgaa gaaatcgttaa aacgtctttc tggctcgtcgt cagcagctgt cttcgtgtgt 720
 tgtttatacac gttgtatata atccacctaa atgtggaagt aaagatgatg tcacaggnnn 780
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnct tcaacgctgt aaaaattacgt 840
 aactctaaaa ctggtaaagt tttagaaaaa acttttaaat ctggtgatgc tttagaagct 900
 gctgcactcg tagaagtaga aatgaactac ctatacaacg atggcgaaat gtggcacttc 960
 atggcccccag aaagcttcga acaaaattgca gtgacaaaaa ctgcaatggg tgatgctgct 1020
 aaatgggttaa aagacgactc aaatgaaaca tgtacaatca tglttattca cggcgttcc 1080
 ttaaacgttaa atgcacctaa cttcgttgta ttgaaagtgt ttgaaactga tccggcgcta 1140
 cgtgtgtgata cttcgtgtgt tnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1200
 ntctgcccgc yaatttgcct aaagctgccc gccttgtagc acagcaagggc aaatttccgt 1260
 aaactctaga agaattgatt gcactaccgc gcattgtgtg ctccagcgca ggtgcactca 1320
 tgtcttttag ttacgtctag ttatggctga ttagcgtagc caacgtgaaa cgcgttttag 1380
 ccogtcttct tgccattgaa gatgacttaa gcaaacacca gcaacgaact gaaatgtgga 1440
 aactggctga agagcttttg cccaccacca gcaactatga tcaactcaac gcgannnnnn 1500
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnttaaaa acactagcgg taagctttaa 1560
 caagattgcc aatgatattc gttggttagc aagtggtcca cgttgcggct tcggcgaaat 1620

```

cogtattctt gaaaaagaac ctggttcaag tatcatgcc aagtaag tga acccgactca 1680
aagtgaagcc atgacccatgg ttgtgtctca agtactttgg aacgata cca ctattaatgt 1740
cgctgtgtct tctgttaact tcgagctcaa tgtatttat ccagtgartt ctataaactt 1800
actcgaactc attcagttgc ttgtgtatgc atgtaatagt tttaatgatc actgtgcagt 1860
agggatcgag ccaaatcggt agaaaaattga tcatttcttg cataatt ctc ttatgttagt 1920
tacggcannnn nnnnnnnnnn nnnnnnnnnn nnnnnnnn ccc gggtatgtac 1980
caaaatacttt gtcctgaagat ggtgacccat tagacgtact tgtgtga act ccaactctcg 2040
ttgtcgcggg ttctgtaact cgttgccggc cagtggggcaa attaaacatg gaagacgacg 2100
gtgtatcgta tgcnnnnn                                     2118

```

<210> 764

<211> 276

<212> DNA

<213> *Acinetobacter baumannii*

<400> 764

```

atgagcgagc taggcttaaa aagcagtggt aagccaaaa aatcagcgcg tacagtgggt 60
gatgtacttg gtaaaatcca cccacatggt gactcggcat gttatga agc catggtaact 120
atggctcagc catttagtta ccgtatctct ttaatogaag gtcaggggaa ctgggggtta 180
cctgatgctc ctaaatcttt tgctgcgatg cgttataccg aagccaa act ctcggcttat 240
agtgaattat tgctgagcga attaggtcag ggcact                                     276

```

<210> 765

<211> 9610

<212> DNA

<213> *Yersinia pestis*

<400> 765

```

tgtaacgaac ggtgcaatg tgatccacac ccaacgcctg aaatcag atc cagggggtaa 60
tctgctctcc tgattcagga gagtttatgg tcaacttttg gacagtt atg gaaattaaaa 120
tcttcgacaa gcagggaatg agtagccggg cgattgccag agaactg ggg atctcccgca 180
ataccgttaa acgttatatt caggcaaaat ctgagccggc aaaatat acg ccgcgacctg 240
ctgtgtcttc actcctggat gaataccggg attatattcg tcaacgc atc cgcgatgctc 300
atctctacaa aatcccgcca acggtaatcg ctgcggagat cagagac cag ggatatcgtg 360
goggaatgac cattctcagg gcaattcatt gttctctctc ggttctc cag gagcaggagc 420
ctgcgcttgc ttctgaact gaacccggag gacagatgca ggttgactgg ggcactatgc 480
gtaaatggtg ctacccgctt caoctgtctg ttgtgtgtct cggatatac cgc gaatgctgt 540

```

```

acatcgaatt cactgacaat atgcgttatg acacgctgga gacotgc cat cgtaatgctt 600
tccgcttctt tgggtggtgt ccgcgcgaag tgtgtatga caatatg aaa actgtggttc 660
tgcaacgtga cgcataatcg accggtcagc accggttcca tctctcg ctg tggcagttcg 720
gcaaggagat gggcttctct ccccgactgt gtgcgccctt cagggca cag actaaaggta 780
agggtggaag gatggtgcag tacaccgta acagttttta catcca cta atgactcgcc 840
tgccgccgat cggatcatcct gtogatgttg aaacagccaa ccgccac ggt ctgcgctggc 900
tgccagatgt cgttaaccaa cgaagacatg aaacatcca ggcctgt ccc tgcagctcgt 960
ggctcgaaga gcagcagctc atgctggcac tgctccggga gaaaaaa gag tatgacgtgc 1020
atcttgatga aaatctgggt aacttcgaca aacacccctc gcatcat cca ctctccatct 1080
acgactcatt ctgcagagga gtggcgtgat gatggaactg caactc aac gactgatggc 1140
gctcgcgggg cagttgcaac tggaaagcct tataagcgca gcgcctg cgc tgcacacaa 1200
ggcagatgac caggaatgga gttatatgga ctctcggag catctgc ttc atgaagaaaa 1260
actggcagct catcaacgta aacaggcgat gtataccgga atggcag cct tccgcgctg 1320
gaaaacgttc gaagagtat acttcacatt agccacgga gcaccgc aga cgaactcca 1380
ctcgttatgc tcaactcact catatgaacg taatgaaat atcgat tac tggggccatc 1440
agggttgagg aaaaaccgat tggcaatagc gatgggtat gaagcag tcc gtgcaggtat 1500
caaaagtctg ttcaacacag cagcagatct gttacttcag ttacta cgg cacacgtca 1560
gggcggttat aaaaagagcc ttcagcgttg agtaatggcc ccccgctc cgc tcatcattga 1620
tgaaatagcg tatctgcgct tcatgacgga agaagcaaa cgtgtct tcc aggtcatcgc 1680
taaacgctac gaaaagagcg caatgatctt gacatccaat ctgcgct tgc ggcagtgga 1740
tcaaacgttc ccggtgtgat cagcactgac ctgacgcatg ctgga ccgta ttctacaca 1800
ctcacatgct gttcaaatca aaggagaaag ctatcgactc agacaga aac gaaaggcggc 1860
ggttatagca gaatcgaatc ctgagtaaaa cgttggtatc atattgg gcc ttatggggag 1920

```

atataagtgg	atcacttttc	atccgtcggt	gacacccgtg	tgaattcaag	tgttccagcc	1980
tgaataaac	gaatgccgga	gatacccggt	catatttttt	acacaaattct	ctaattccgga	2040
caaggtcgta	ggctcgttata	ggaaaattct	tagcaccatt	coggaaacaat	cagaaacaga	2100
ggccatgaac	gactgacaac	attacgataa	taaaaaacgc	accggggcca	gacattcccc	2160
ctaotgatta	aacacgcggg	acttgtccac	ggaaocggtct	ttttaaacgg	acacacagctc	2220
tgagtagaca	taactgtcac	gatgatgcag	gatctagcga	agagtgtgag	acaggtttccg	2280
ggaaactgtgg	tgaaccatag	ctcaatatct	gagtgagggc	ataccggaaa	cgcgctcaga	2340
ttcgttgttaa	cgcgatttttc	cgtaccgggc	aattttttca	gttgtttttt	cggttcaatgt	2400
cgctcgaac	gtctcagagc	cgtttcocgc	atctgatgct	acgcaaaacca	ttcccatggt	2460
cagttgcagc	coggaaaacac	gcgggtgtgc	ttttagcgta	tcgacgggac	ggcgtcgaga	2520
gaaacaaaa	acagattgttg	tactcagcca	gttgtttttac	agacaagcaat	ggcgagattt	2580
gaaaagaatg	cgtacttttc	ggaaagtcca	gaaaccatgt	gtcagacttc	gttctccccc	2640
ttccgggtga	atgtttttgt	catccgtcca	gaaatctctt	tataacgatt	actccatttc	2700
aggatttttt	atgtggcggt	tactacagcg	aggatatcca	aaggcaaaaa	aatccccggg	2760
aacaggcgga	acocgggacg	ggggagaaag	aatcgctaaa	taattttctgt	agttgtattt	2820
cccactcgtg	ctactgcgaac	gggatgaatt	tgocgcaatt	tatcccgtta	aaacaatcgt	2880
atgtactcac	actccacata	tcactgacgg	agcaccaacg	aatagtgaac	aaacacaacac	2940
aaactcgctg	gaatatggcg	agatttatca	gaagccagag	ctcgaactgt	cttgaaaaaa	3000
tggatgctct	ggatgcgcag	gagcaggcgg	ccatgtgtga	acgactgcac	gaactcgcgg	3060
aagaactccc	gacacagcgc	caggctcgct	ttgaagccga	aagtgaaaaca	ggaaacataac	3120
gaagctcccg	gaagcgggtca	cagcttctgt	gtgaacggat	gcggcgagcg	gacaagcccg	3180
tcaggcgccg	tcaggcggtt	tttagcgggt	tcggggcgca	gccactgacc	agtcacagtg	3240
ctagagcgga	gtgtatactg	gcttagtcat	gcggcatcag	tgccgattgt	atgaaaagtg	3300
caccatgtac	gggtgtaaat	gcgcacagga	tcgctaagga	gaacatacgag	atgcgcgatc	3360
ttctccgctt	ctcgcgtcac	tgaotcgtg	gcctcgttgc	ttcggctgcg	gcgagcgggt	3420
ttctgtcaat	caaaagcggg	gatactgtta	tcacacacat	cagggcgata	gcggcgaaag	3480
aacatctgag	caaaaaacga	agaccccgga	aaagcccgcg	coggagcggc	tttttccata	3540
gtctccgcgc	atcgacgag	catcacaaaa	atcgacgctc	aagtccaggg	tggcgaaaac	3600
cgacaggaat	taaaagatacc	aggcggttcc	ccocgggaag	tcctctcgtg	gctctcctgt	3660
tcocagacgc	cgcgttacgc	gatacctctc	cgctttcttc	ctctcgggaa	gcgtggcgct	3720
ttctcattag	tcacgctggt	gttatctcag	ttcgggtgtg	tgctgttcgt	ccaagctggg	3780
ctgtgtgcac	gaacccccgc	ttcagccoga	ccactgcgcc	ttatccggta	actatcgctt	3840
tgagttccaa	cgggtaaagc	acgactttac	gccactggga	gcagccattg	gtaaactgaaa	3900
agtggaattta	gatacgcaga	actcttgaag	ttgaagcctt	atcgcgcgta	caotgaaagg	3960
acagcatttg	gtatctgtgc	tcactttaag	ccagctacca	cagggttagaa	agcctgagaa	4020
actctaaacc	ttogaagaag	cccacgcctg	agaaocgtgg	ttttttcgtt	tacaggcagc	4080
agattacgcg	cagaaaaaaa	ggatctcaag	aagatccttt	gatctttctt	actgaattgc	4140
gctcccgatc	agttgcacgag	aagattatga	tggggttcta	tggtgtattg	tcgogttaaca	4200
cccatgtttac	ttgaggttgt	atgtagtctg	tgtagaatta	tacacataag	gtataaaact	4260
ctcttttttt	tcaatatgca	attggaagtt	cattgactac	ataaatagat	tatttccaaat	4320
attttttttt	tgtaaagaaca	ggatggggag	gggaatgac	toaaagtatt	tttgtctggc	4380
ctctcatatt	ttatcatcaa	gtggccttgc	agaaaaaac	acataacag	caaaagacat	4440
tttcgaaaa	ctagaattaa	atacctttgg	caattcattg	ttctatggca	tcatagggaa	4500
acagacaacc	ttcagaocaa	cgcagtttac	aaatattaaa	agcaaacaca	aaaaacacat	4560
tgcacttatc	aataaagaca	actcatggat	gatataccta	aaaatactag	gaattaaag	4620
agatgagtat	actgtctggt	ttgaagattt	ctctctaata	agaccgccaa	catatgtagc	4680
catacatcct	ctactataaa	aaaaagtaaa	atctggaaac	tttatagtag	tgaaaagaat	4740
aaagaaatct	atccctgggt	gcactgtata	ttatcattaa	tagcaagccc	ctacattata	4800
tgagggggctc	atgtgttattt	taacaatacca	ctatcgatat	ctttttgcac	cagagcgccc	4860
ttcgttgtac	gtctgtcaga	cattccatca	acaaatattt	taaaaagcgt	tacaaggcca	4920
ttccagttct	ttgcgataaac	tttatcccat	actgtgggag	cagttctgga	taactctaac	4980
cccttttgat	atccaaataga	caaccagtcg	gtacgggttc	toaacccgta	actcgtcgac	5040
cgaagacaga	tattagcgtc	attgaaaaga	ccctcaattc	tatgtcgaaa	tttatcaata	5100
taaatattga	ataaagagtg	agcttcatta	tcgaagaagc	tcagagcggt	gttcttcaact	5160
ttatcataag	ccctcctccc	tcgaagcata	taatacccat	caagttctatc	tgcaatatac	5220
tgagggaac	cgtcaattcaa	taaatctcgt	ttgcttcgct	gaccacaggt	aaccccgaaa	5280
ccgaattgtaa	caccgggtact	gttaaaataa	tcgtactag	tactagacgg	aaaatgactt	5340
tgccgatttaa	acccttcaaaa	accattactg	gagaaaaat	cgtgtgtcaac	aatatttaac	5400
gaacagcgtg	aaaatttccct	cagttgacta	atatgttcaa	agtttaagtg	agttgtgtcc	5460
gtcaggaaga	tcgcgatttcg	gttattatct	gaagtgtcct	cgcttctctt	cttatcgaga	5520
tgctcaaatag	atttcggcag	cgttccctca	agaaccatga	cacggttacac	tttccacagc	5580

tottttttct	gacctgtttc	aacagttatt	ttctgttctg	aagacacggt	cocttcagtt	5640
tttgaattct	taactttctg	goggatctta	tttgaattatt	caactgtcttt	ctccatctcc	5700
gtatcaatcg	gaacccocat	aatgtacatc	agtttataat	taactcggcc	agggagatcc	5760
acataatgtg	gtaatgcatt	tgtaatcgaa	ttagcttcaa	aattttgctct	gtaactgctt	5820
aatgtacttc	cggaaaaagag	aaaagccgga	acaccacctg	aacattccac	taccattgta	5880
tctgacataa	aaattctctc	ttaacacata	aaaaaacatc	aagttaaaaa	aaaaactcgt	5940
acataaaac	actgtttttt	tgtacagtaa	taaaattacg	ccgctttatt	ttctctgtca	6000
ataattgaa	atttcatttt	tgtgatctga	atcactctta	taaaaactag	gaaggagaca	6060
ttcgcagcag	aaaaacagca	ccgggttaaca	tcagaaaaaa	acagaaaagga	gataacgtga	6120
gcacaaacaa	atctggtcgc	caccgactga	gcacaaacaga	caaacgcctg	ctgctgtcac	6180
tttgtctgtc	cggatgcagaa	gaacggacag	ccctgtgacct	catccagaaa	caagtttaca	6240
cactgcagca	cgccgacctg	cgccatctgg	tcagtgaatc	cagttaacgtg	ctgggacagt	6300
cacaggccta	cgatgcgatt	taccaggcga	gaocgattcg	ctctgcgcctg	aaataacctga	6360
gcggaaaaaa	accggaaggg	gtggaacccc	gggaagggca	ggaaacggaa	gatttaccat	6420
aaactccggt	atcagtagca	toggctcaac	gctcgtttgc	ggatctgaaa	aattcgcctca	6480
aaagatcata	tttccctgga	tattttccac	cgtttcttat	gtgagcaaat	tcacataatt	6540
ctctcagcag	acgagaaaac	ggatctcgat	tattgtttaa	tatttttaca	ttattaaaaa	6600
tgaatttaga	taatcagata	caataaatat	gttttctgtc	atgcagagag	attaagggtg	6660
tctctagaag	aaaagtctct	ttgtggcaac	cattataact	attctgtcgc	ggagtgctaa	6720
tgcagcatca	tctcagttaa	taccacaaat	atccctgac	agctttacag	tgcagcctc	6780
caccgggatg	ctgagtgtaa	agtcctcatga	aatgtcttat	gacgcagaaa	cagcgtaaga	6840
gatcagccag	ttagactgca	agatcaaaaa	tgtcgtctatc	ctgaaaaggtg	atatattcctg	6900
ggatccata	tcattttctg	ccctgaatgc	cagggggttg	acgtctctgc	cttccgggtc	6960
aggttaattg	gatgactcag	actggatgaa	tgaanaatcaa	ctctgagtga	cagatcactc	7020
atctcatctc	gtcacaattg	ttaatcatgc	caatgaatat	gaacctcaatg	tgaagggtc	7080
gttactccag	gtgagaaatt	ataaagcagg	tataacagca	ggatcatcag	aaaacgcttt	7140
cagttgggca	gtcacagggt	gttcatatag	ttataataat	ggagcttata	ccggaaaact	7200
ccggaagaag	gtcgcggttaa	taggtttataa	ccagcgcttt	cttatggcat	attttggact	7260
tgcagccagc	tatcgcatata	atgattttga	gttaaatgca	tttatttaatt	ctacogagatt	7320
ggctcgggca	catgataatg	atlgagcaata	tattgagagat	cttactttcc	gtgagaagac	7380
atccgctctc	cgttattatg	tacocgttaat	taacgctgga	tatttatgtca	caactaatgc	7440
caaaagctct	cggaatttta	catcacagtaa	atatgatgag	ggcacaagag	gtactcagag	7500
cattgataag	aatgtgtgag	attctgtctc	tattggcgga	gatgctgcgc	gtatttccaa	7560
taaaaattat	actgtgacag	cggtctcgca	atatcgcttc	tgaanaatcac	agatcatctc	7620
tctcttttca	ttctccoccta	goggggagga	tgtctgtgga	aaggaggttg	gtgtttgaoc	7680
aaactctcag	tgtgtgaaaa	atccactttt	tcaccataat	gaacgggggc	tacattctgtt	7740
gttttgcctt	gacattttcc	acgtctttca	gggcattggag	aaggtcacaat	tagacattgga	7800
acgtctactc	ctttctctgta	ggaagctcaa	catccaaagt	taatttgctc	ccatttgctt	7860
aaacgtaaag	cttttaacgtc	gccagcttta	aatcaatttc	gcgctgctcc	agctttgtta	7920
ctctgctgct	gotttataccc	atcgctcag	caactttggt	tttgtataaac	tggagttctt	7980
cacgcatacat	ctcgaaagcg	acctaagaag	ttactctcatc	tgccattttc	tttaactgtc	8040
tctggttttc	agagtgaagca	ctggcaatca	ctcatcttaa	tgttctcatt	acttgcctct	8100
cagttgtgtc	agattgtcgtg	taaaattcatc	ctcagctata	cgccacagtt	tttccataaaa	8160
cgccttaata	ttacttttat	ctctctgcaca	aagaacgata	gcocagcaag	tccgtatcgaa	8220
cgcataaaag	gctcttatcg	gaocggcaga	aaactgcagc	cgaagctctt	tcattttttt	8280
gtaccagaga	ctcttccagg	tatcgccata	tggcctgggt	aactcaggctc	cgtaaacctg	8340
tagctttttc	aaatcagaca	aaactctttc	ctgaagagcg	ctctttctgt	catttagcca	8400
gtcgtcaaat	ctcggtgctaa	aaagtacacat	ccactgtctc	aaacctataa	tgactgtgct	8460
accccaactaa	caatataccc	tacgagttat	attttcaaga	aaagctggct	atttacaata	8520
acggcaattt	gtcagcaacc	ctgaattgcg	ttcagcgoga	ctacggcgaac	agacagccaa	8580
aaatagcaac	aaactctccg	aaaaacccgc	cgcatcgccg	ctgataaatt	ttaaccttat	8640
catatctat	gcagccagcg	gaatoacgaa	cgaattgcct	gcctgatgta	actgaaacgg	8700
gtgttttttc	ctgattttgt	ggcggtggaa	gacggaaacat	gaacggggaa	acagaaattca	8760
tgccagatga	cgcgatctga	gcaattaaag	caaaaacagc	caacaaagag	acgcaggaat	8820
cgcgcocgga	tatgttttaa	cgcgattttc	agactcagac	aaattcagca	gaattgctact	8880
cccttccagc	ggctgatggg	gaatacatgc	gtatccgctc	tgagtcaatt	cttgcgtctg	8940
ccacagctct	gtctgtggc	agctttcgcc	gtgcgggaaa	ctgtctttaa	acgctcccca	9000
aaggctctct	aacccagaag	caacaaaaaa	caggccattca	agtaaatcgc	gttataaacac	9060
gtctgatgga	ttctgcacaa	aaaaagctcc	taattgagca	gggactgtgc	aacccagatga	9120
atagcgtcta	taataaagta	agaataacac	caggtactct	tcagaaaaga	gattatacca	9180
cgcgacacaa	taatcaacag	taaaaaacaa	caacctgat	tttttttttt	ttcttttttt	9240

```

gataaaaaca aaattaaaga aataattaat cagaacattc ctt aacttca gggcattgcc 9300
tgtgttccat tttgtgatta gtctgaaact tccgaaggtg gat aacaccc ggtatttttt 9360
tgctcacata aagcccctcc ttcaggcaga ggggcttttt ctt tgccacc acataaaaaa 9420
ggccctcaca ggaggtgttc tgtgaggcgc tatgataagg act gaatcga ttggttaat 9480
gtotagtccg gacttttgca tctccgaata taaaaccctg ttt aacggca tgcaaaacca 9540
aaaaataaaa atgtgacatc gcaatgccag ataataattga cgc atgaggg aatgcgtacc 9600
ccgacccctg

```

<210> 766

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> Calibration Polynucleotide

<400> 766

```

tttaagtccc gcaacgagcg caacccttga tcttagttgt tta gttgggc actctaaggt 60
gactgccggt gacaaaccgg aggaaggtgg ggaatgacgtc aa 102

```

<210> 767

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223> Calibration Polynucleotide

<400> 767

```

tagaacacgg atggcggaag cgactttctg gtctgtaact gac actgaga aagcgtgggg 60
agcaaacagg attagatacc ctggtagtcc acga 94

```

<210> 768

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Calibration Polynucleotide

<400> 768

```

tggattagag accctggtag tccacgccgt aaacgatgag tgctaagtgt tagaggcctt 60
tagtgcgtgaa gttaacgcat taagcactcc gcctggggag tacggcca 108

```

<210> 769

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> Calibration Polynucleotide

<400> 769

```

tttcgatgca acgogaagaa ccttaccagg tcttgacatc ctctgacaac cctagcttct 60
ccttcggggc cagagtgcga ggtggtgcac ggctgtcgtc agctcgta 108

```

<210> 770

<211> 95

<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 770
tctgacacct gcccggtgct ggaagggttaa ggaagaggggt tagcgtaact ctgaactgaa 60
gcccaggtaa acggcgggcg taactataac ggtca 95

<210> 771
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 771
tctgttctta gtacgagagg accgggatgg acgcacgggt accagttggt ctgcaaaggg 60
catagctggg tagctatgtg cggaagggat aagtgcctgaa agcatctaa cgcgaaa 117

<210> 772
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 772
tgattattgt tatcctgtta tgccatttga gatttttgag tggatttga gttattgttc 60
caggattaat tgcaaatata attcaagac aagggtctaca 100

<210> 773
<211> 112
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 773
tcgaagtaca atacaagaca aaagaaggta aaatta.ctgt tttaggggaa aaattcaaga 60
aatatagaag tgatggctaa aaatgtagaa ggggtcttga agccgttaac aa 112

<210> 774
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 774
ttgctcgtgg tgcacaagta acggatatta caatca.ttgt tgttgcagct gatgacggcg 60
taataaacag ttgaagcaat taacctgctg aaagcagca 100

<210> 775
<211> 114

```

<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 775
tagctttttgc atattatatac gagccacagc atcgtgatgt tttacagctt tatgcaccgg 60
aagctttttaa tggataaatt taacgaacaa gaaataaatc tatccttgga agaa 114

<210> 776
<211> 116
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 776
tgacctacag taagagggttc tgtaatgaac cctaatagac atccacacgg tgggtggtgaa 60
ggtagatctc ctatcggaag gtccacgtac tccatggggc aaaccagcac ttggaa 116

<210> 777
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 777
tccacacggt ggtggtgaa gtagatctcc tatcggaag tccacgtact ccattgggga 60
aaccagcaca 70

<210> 778
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 778
ttatcgctca ggcgaactcc aacctggatg atgaaggccg ctttttagaa ggtgacttgt 60
cgtagcaaa gcaatccag ca 82

<210> 779
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Calibration Polynucleotide

<400> 779
tgggcagcgt ttcggcgaaa tggaagtggc tcgaagcgta tggcgcttcg tacgtgctgc 60
aggaaatggt gaccgtcaag tcggaca 87

<210> 780

```

<211> 97
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Calibration Polynucleotide

 <400> 780
 tcaggagctgc ttcaactcga totacatgat ggccgaccgc ccgggggttcg gcggtgcaga 60
 ttgctcagct ggccggcatg cgtggcctga tggcgta 97

 <210> 781
 <211> 117
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Calibration Polynucleotide

 <400> 781
 ttgtggcaggt atgcgtggtc tgatggccaa tccatctggt cgtatcatcg aacttccaat 60
 caagtttccg tgaagggtta acagtaactg agtacttcat ctcaaccac ggtgcga 117

 <210> 782

 <211> 98
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Calibration Polynucleotide

 <400> 782
 tcaagcaaac gcacaatcag aagctaagaa agcgcaagct totggaaagc acaaatgcta 60
 gttatggtag agaatttgca actgaaacag acgtgcaa 98

 <210> 783
 <211> 99

 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Calibration Polynucleotide

 <400> 783
 tccacacgcc gttcttcaac aactaccgtg ttctaettcc gtacgacgga cgtgacgggc 60
 tcgatcgagc tgccgaagga caaggaaatg gtgatgcc 99

 <210> 784
 <211> 111
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Calibration Sequence

 <400> 784
 tcgtggcggc gtggttatcg aaccatgct gacgatcaa tggtaactgc acaccgcccc 60
 ccaagctgcg gattgaagcc gttagaagc gcgacatcca gttcgtaccg a 111

<210> 785
 <211> 2100
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Combination Calibration Polynucleotide

```

<400> 785
gaagtagaga tatggaggaa caacagtgcc gaagcgact ttctggtotg taactgacac 60
tgagaaagcg tggggagcaa acaggattag atacctggg agtccacgcc gtaaacgatg 120
agtgctaagt gtagaggcc tttagtgtg aagttaaagc attaaagcaot cgcctggggg 180
agtacggccg caagcgtgaa actcaaagga attgacgggg cacaagcggg ggagcatgtg 240
gtttaattcg aagcaacggc aagaacctta ccaggtcttg acatcctctg acaacctgat 300
cttcctcttc gggagcagag tgacaggtgg tgcattggtg tcgtcagctc gtgtcgtgag 360
atgttgggtt aagtcccgca acgagcgcaa ccttgatctt tagttgttta gttgggcact 420
ctaaggtgac tgccggtgac aaacgggaag aaggtgggga tgacgtcaaa tcatcatgcc 480
ccagtaccgt gagggaaaag tgaaaaagc cccggaaggg gagtgaagaa gatcctgaaa 540
ccgtgtgcca tagtcagagc ccgttaacgg gtgatggcgt gcccttttga gaatgaacgg 600
cgcagttata agatccgtag tcaaaaagga aacagcccg accgccagot aaggtcccaa 660
agtggtgtatt gaaaaggatg tggagttgct tagacaacta ggatgttggc ttagaagcag 720
ccaccattaa aagagtatag ggggtgacac ctgcccgtg ctggaaggtt aaggagaggg 780
gttagcgtaa cctotgaact aagcccagtt aaacggcggc cgtaactata accgtcctaa 840
ggtagcgaaa gaaatttgag aggagctgtc cttagtaca gaggacccgg atggagcac 900
cggtaaccgt tgtcttgcca agggcatagc tgggtagcta tgtcgggaag ggataagtcg 960
tgaaagcatc taagcatgaa gcccccctca agatgagagc agtaaaacaa gcaaacgcac 1020
aatcagaagc taagaaagcg caagctcttg gaagcaca aa atgctagtta tggtcagaaa 1080
tttgcgaactg aaacagacgt gcattgctgt aaatttgcga aagcttttgc atattatctc 1140
gagccacagc atcgtgatgt tttacagctt tatgcacggg aagcttttaa tggataaatt 1200
taacgaacaa gaaataaatc tatccttgga agaactttaa gatcaacgga tgcgtggcaag 1260
atatgaaaaa taagataaaa cagcactatc aacactcgag cgattcttta tctgaagaa 1320
gaagagcgat gaaaacaacg aagtacaata caagcamaaa gaaggtaaaa ttaactgttt 1380
aggggaaaaa ttcaagaaat atagaagtag tggctamaaa ttagaagagg gtcttgaagc 1440
cgttaacagc tggtatggcg accgtggcgg cgtggttacc gaacccatgc tgaccgatca 1500
atggtacgtg cacacggccc ccaaaagtgc cgttgaaagc cgtagagaac ggcgagatcc 1560
agttcgtccc taacacgtac ggcaactcgt ttatcgtcca ggcgaactcc aacctggatg 1620
atgaaggccg ctttttagaa ggtgacttgt cgtagcaaa gcgaaatcaag cctgtttagc 1680
cacaactatg cgtgctcgtg gtgcacaagt aacggatatt acaatcattg ttgttcgagc 1740
tgatgacggc gtaataaaca gttgaagcga ttaaccatgc gaaagcagca ggaagtacaa 1800
ctttactcag cttgctggta tgcgtggtct gatggcgaat ccatctggtc gtatcatcga 1860
acttccaatc aagtttcgtg gaaggtttaa cagtaactga gtacttcatc ttaacgcatg 1920
gtgcgcgtaa aggtcatggg agtaagacct acagtgaag gttctgtaat gaacctaat 1980
gacctccac accgtggtgg tgaaggtaga tctcatcgc gaaagtcac gtactccatg 2040
gggtaaacca gcacttggat acaaaaacag ccgagttcgg cggccagcgc ttcggtgaaa 2100

```